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GenCore version 5.1.7
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OM protein - protein search, using sw model

February 15, 2006, 13:07:33 ; Search time 233 Seconds (without alignments) 2240.734 Million cell updates/sec Run on:

US-10-659-055-3 4020 1 ADPGCSHHHHHHSRKTYTLT......AHQHIYTHMSHFIKQCFSLP 740 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P27487 h dipeptidy	Q53tn1 homo sapien	Q5r7g7 pongo pygma	Ω,	Q9n2i7 f dipeptidy	8	P14740 r dipeptidy	P28843 m dipeptidy	Q75s83 agkistrodon		gallus		xenopus	homod	homo	rattr	_	Q91651 xenopus lae		Q48309 tetraodon n	Q8n608 homo sapien		Q6inb7 xenopus lae	Q6nxk7 mus musculu	P42658 homo sapien	Q7psf9 anopheles g	Q5is50 pan troglod			Q9vmm2 drosophila	P42659 bos taurus
SUMMARIES	er .	DPP4_HUMAN	Q53TN1 HUMAN	Q5R7G7 PONPY	DPP4 BOVIN	DPP4 FELCA	DPP4_PIG	DPP4 RAT	DPP4 MOUSE	Q75S83 AGKHB	Q75S82_AGKHB	Q5ZI81_CHICK	Q641D6 XENLA	P70092 XENLA	Q53TP5_HUMAN	SEPR HUMAN	Q8R492_RAT	SEPR_MOUSE	091651 XENLA	Q4RQJ4_TETNG	Q4S309_TETNG	DPP10_HUMAN	DPP10_RAT	Q6INB7_XENLA	DPP10 MOUSE	DPP6 HUMAN	Q7PSF9 ANOGA	DPP6 PANTR	Q9QVT8 9MURI	DPP6 RAT	Q9VMM2 DROME	DPP6_BOVIN
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Query	Match	98.0	98.0	97.3	89.2	88.6	88.3	•	84.3	62.7	62.7	62.7	58.4	58.0	54.1	53.9	53.7	53.7	52.6	49.6	45.3	30.4	30.1	29.9	29.4	28.1	28.0	27.9	27.8	27.8	27.7	27.5
	Score	3939	3939	3910	3585	3560	3548	3408.5	3390	2520.5	2519.5	2519	2348	2331.5	2115	2168	2160.5	2158.5	2115	1992.5	1819.5	1222	1210	1202.5	1183	1129	1124	1121	1118	1116	1112.5	1106
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ALIGNMENTS

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Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
Latchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of sucrase-isomaltase and dipeptidylpeptidase IV in human small intestine and colon.",
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Darmoul D., Lacasa M., Baricault L., Marguet D., Sapin C., Trotot P.,
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MEDILINE=96067599; PubMed=7487939;
Boehm S.K., Gum J.R. Jr., Erickson R.H., Hicks J.W., Kim Y.S.;
Boehm S.K., Gum J.R. Jr., Grickson R.H., Hicks J.W., Kim Y.S.;
"Human dipeptidyl peptidase IV gene promoter: tissus-specific regulation from a TATA-less GC-rich sequence characteristic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93210468; PubMed=8096237; DOI=10.1084/jem.177.4.1135;
Morrison M.E., Vijayasaradhi S., Engelstein D., Albino A.P.,
Houghton A.N.;
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                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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J. Exp. Med. 177:1135-1143(1993).
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Biochem. J. 311:835-843(1995).
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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--- SUBGILIULAR LOCATION: Type II membrane protein. Also exists in a
            CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 35-771, HOMODIMERIZATION, AND
                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 39-766, HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                               CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 39-766, HOMODIMERIZATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eoluble form.
--- TISSUB SPECIFICITY: Expressed in the poorly differentiated crypt cells of the small intestine as well as in the mature villous cells. Expressed at very low levels in the colon.
--- PTM: The goluble form (SDPP) derives from the membrane form (MDPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by proteolytic processing.
SIMILARITY: Belongs to the peptidase 89B family. DPPIV subfamily.
                                                                                                                                                                               N-GLYCOSYLATION SITES.
PubMed=12483204; DOI=10.1038/nab882;
Rasmussen H.B., Branner S., Wiberg F.C., Wagtmann N.;
"Crystal structure of human dipeptidyl peptidase IV/CD26 in complex
          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 35-771, HOMODIMERIZATIC N-GINTCOSYLATION SITES.

N-GINTCOSYLATION SITES.

PubMed=12646248; DOI=10.1016/S0006-291X(03)00258-4;

Hiramatsu H., Kyono K., Higashiyama Y., Pukushima C., Shima H., Sugiyama S., Inaka K., Yamamoto A., Shimizu R.;

"The Erructure and Function of human dispeptidy peptidase IV, possessing a unique eight-bladed beta-propeller fold.";

Biochem. Biophys. Res. Commun. 302:849-854(2003).
                                                                                                                                                                                                                                                                                                                N-GLYCOSYLATION SITES.
PubMed=12906826; DOI=10.1016/S0969-2126(03)00160-6;
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"Structural basis of proline-specific exopeptidase activity as observed in human dipeptidyl peptidase-IV.";
Structure 11:947-959(2003).
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EMBL; U13710; AAB60646.1; JOINED; Genomic_DN
EMBL; U13711; AAB60646.1; JOINED; Genomic_DN
EMBL; U13712; AAB60646.1; JOINED; Genomic_DN
EMBL; U13713; AAB60646.1; JOINED; Genomic_DN
EMBL; U13714; AAB60646.1; JOINED; Genomic_DN
EMBL; U13715; AAB60646.1; JOINED; Genomic_DN
EMBL; U13715; AAB60646.1; JOINED; Genomic_DN
EMBL; U13715; AAB60646.1; JOINED; Genomic_DN
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Struct. Biol. 10:19-25(2003).
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                                                                                                                                                                                                                                                                                                                                        Wilson R. K.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
R EMBL; ACOROSO63; AAX93179.1; -; Genomic_DNA.
R EMBL; ACOROSO63; AAX93179.1; -; Genomic_DNA.
R GO; GO:0016020; C:membrane; IEA.
GO; GO:0004274; F:catalytic activity; IEA.
GO; GO:0004274; F:prolyl oligopeptidase IV activity; IEA.
GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR00247; Peptidase_S9.
R InterPro; IPR00375; Peptidase_S9.
R InterPro; IPR00375; Peptidase_S9.
R InterPro; IPR00379; Ser_estra.
R Ffam; PF00326; Peptidase_S9; I.
R PROSITE; PS00708; PRO_ENDOPEP_SER; I.
                                                                Ozanich A., Stoneking T., Hawkins M., Sapetti L.;
"The sequence of Homo sapiens BAC clone RP11-178A14.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                databases
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Hypothetical proteIn; Transmembrane.
766 AA; 88279 MW; 5PB4A2C6662D6117 CRC64;
                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                the EMBL/GenBank/DDBJ
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SEQUENCE 766 AA; 88279 MW; SF
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                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Waterston R.H.;
Submitted (NOV-1999)
                                                                                                                                                                                                                                                          Waterston R.;
Submitted (SEP-2000)
                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
NCBI_TaxID=9606;
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Best Local S
Matches 728
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
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Last sequence update)
Last annotation update)
                                                              98.0%; Score 3939; DB 1;
100.0%; Pred. No. 2e-259;
iive 0; Mismatches 0
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EMBL; M74777; AAA51943.1; -; mRNA.
EMBL; BC013329; AAH13329.2; -; mRNA.
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13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein DPP4.
                                                                                  Best Local Similarity 100. Matches 728; Conservative
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Q53TN1;
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IKQCFSLP 766
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DPP4_BOVIN STANDARD;
P81425; Q88MG8;
15-DEC-1998 (Rel. 37, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2005 (Rel. 48, Last annotation update)
Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP
Dipeptidyl peptidase Complexing
Protein) (ADCP-I) (Activation molecule 3) (ACT3) (Will) (Contains:
Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase IV membrane form) soluble form)
                                                                                                                                                                                               VINATSIQITAPASMLIGDHYLCDVTWATQERISLQMLRRIQNYSVMDICDYDESSGRWN
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                              NGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
                                                                    218 NGTFLAYAQFNDTEVPLIEYSFYSDBSLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
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MEDLINE=22067734; PubMed=12073152; DOI=10.1007/800251-002-0456-6;
Lee S.-U., Park Y.-H., Davis W.C., Hamilton M.J., Naessens J.,
Bohach G.A.;
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-17.
TISSUE=Thymus;
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Bos taurus (Bovine).
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RA Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.;
RESUDING CREGOIS CAH92293.1; -; mRNA.
BENDING CREGOISO; CAH92293.1; -; mRNA.
BENDING CREGOISO; CAH92293.1; -; mRNA.
BENDING GO: 00016020; c:membrane; IEA.
BOR GO; GO: 00016020; c:membrane; IEA.
GO; GO: 0001477; P:minopoptidase activity; IEA.
BOR GO; GO: 0001477; P:minopoptidase activity; IEA.
BOR GO; GO: 0001477; P:prolyl oligopetidase activity; IEA.
BOR InterPro; IPR002469; Peptidase_S9.
BOR InterPro; IPR003175; Peptidase_S9.
BOR InterPro; IPR003175; Peptidase_S9.
BOR Fam; PF003176; Peptidase_S9; I.
BRAM; PF003176; Peptidase_S9; I.
BRAM; PF003176; Peptidase_S9; I.
BRAM; PF003176; Peptidase_S9; I.
BRAM; PF003176; PPC ENDERPERER; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                      EYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMMYTDEDHGIASSTAHQHIYTHMSHF
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                                                                    DGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                                                                                                  VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
                                                                                                                                                                                                                                    VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
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97.3%; Score 3910; DB 2; Length 765;
Best Local Similarity 99.2%; Pred. No. 1.9e-257;
Matches 722; Conservative 2; Mismatches 4; Indels
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765 AA; 88038 MW; 6F81ECD98C3D2397 CRC64;
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QSR7G7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.
SUBUNIT: Homodimer.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a soluble form (By similarity).
TISSUE SPECIFICITY: Intestinal epithelium, dendritic cells and seeveral immune system tissues prof.
FYM: The soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic processing (By similarity).
SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
MEDLINE=22021197; PubMed=11981816;
DOI=10.1002/1521-4141(200205)32:5<1472::AID-IMMU1472>3.0.CO;2-Q;
Gliddon D.R., Howard C.J.;
"CD26 is expressed on a restricted subpopulation of dendritic cells in
                                                                                                                                                                                            DOI=10.1128/IAI.69.11.7190-7193.2001;
Lee S.-U., Ferens W., Davis W.C., Hamilton M.J., Park Y.-H., Fox L.K.,
Naessens J., Bohach G.A.;
"Identity of activation molecule 3 on superantigen-stimulated bovine
                                                                                                                                                                                                                                                                                                                                                                                                                     calf
                                                                                                                                                                                                                                                                                                                                                                                         Ben-Shooshan I., Parola A.H.,
"The CP-I subunit of adenosine deaminase complexing protein from calf kidney is identical to human, mouse, and rat dipeptidyl peptidase IV.";
Biochem. Physiol. 1198:289-292(1998).
--- FUNCTION: Removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is proline. Binds and regulates the activity
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
MEDLINE=98293306; PubMed=9629661; DOI=10.1016/S0305-0491(97)00327-1;
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GICNAc. . ) (By similarity).
N-linked (GICNAc. . ) (By similarity).
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Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase;
Protease; Serine protease; Signal-anchor; Transmembrane.
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Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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EMBL; AY056834; AAL23628.1; .; mRNA.
HSSP; P27487; 1PF0.
SMR; P81425; 38-764.
MEROPS; S09.003; ...
InterPro; IPR001375; Peptidase S9.
Pfam; PF0030; DPPIV N; T.
Pfam; PF0030; Peptidase S9.
InterPro; IPR00130; Peptidase S9.
Pfam; PF0030; Peptidase S9.
InterPro; IPR00130; Peptidase S9.
InterPro; IPR00130; Peptidase S9.
InterPro; IPR00130; Peptidase S9.
INTERPROSE PEPTIDASE SPECIAL 
                                                                             vivo.";
Bur. J. Immunol. 32:1472-1481(2002)
                                                                                                                                                        TISSUE=T-cell;
MEDLINE=21482004; PubMed=11598101;
                                                                                                                                                                                                                                                                                                Infect. Immun. 69:7190-7193(2001).
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PROTEIN SEQUENCE OF 1-24.
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AD DPP4 PIG
TO P2241; Q8662;
DT 01-AUG-1991 (Rel. 19, Created)
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WEDLINE-20094000; PubMed=10630304; DOI=10.1007/8002510050616;

MEDLINE-20094000; PubMed=10630304; DOI=10.1007/8002510050616;

MISAHIMLTA Y., MIYAZAWA T., Ikeda Y., Izumiya Y., Nakamura K., Sato E., MikaH. T., Takahashi E.;

"Molecular Cloning and sequencing of a CDNA encoding the feline T-cell activation antigen CD26 homologue.";

"Molecular Cloning and sequencing of a CDNA encoding the feline T-cell mmunogenetics 50:366-368(1999).

"Immunogenetics 50:366-368(1999).

"Immunogenetics 50:366-368(1999).

"Immunogenetics 50:366-368(1999).

"Immunogenetics 50:366-368(1999).

"Immunogenetics 50:366-368(1999).

"Coloration antigen CD26 homologue.";

"CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-CATALYTIC ACTIVITY: Release of an N-terminal dipeptide COC Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided CATALYTIC ACTIVITY: Release of an N-terminal dipeptide COC Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided CATALYTIC ACTIVITY: National Activity of the membrane protein. Also exists in a soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic processing (By similarity).

"In The soluble form (SDPP) derives from the membrane form (MDPP) by proteolytic processing (By similarity).

"In The soluble form (SDPP) derives from the membrane form (MDPP) coloration the peptidese SSB family. DPPIV subfamily.
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (By similarity).
N-linked (GlCNAc. .) (By similarity).
                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 46, Last annotation update)
13-SEP-2005 (Rel. 46, Last annotation update)
19-SEP-2005 (Rel. 46, Last annotation update)
10-SEP-2005 (Rel. 46, Last annotation u
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InterPro; IPR002471; Pept S9 AS.
InterPro; IPR002469; Peptidase_S9.
InterPro; IPR000375; Ser estrs.
InterPro; IPR000379; Ser estrs.
Pfam; PF00030; DPPIV N; I.
Pfam; PF00326; Peptidase_S9; 1.
PROSTIE; PS00708; PRO ENDOPEP_SER; 1.
Aminopeptidase; Glycoprotein; Hydrolase; Protease; Serine protease;
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HSSP; P27487; 1PFQ.
SMR; Q9N217; 38-765.
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(Potential).
(By similarity).
(By similarity).
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N-linked (GlcNAc. ..) (By N-linked (GlcNAc. ..) (Pot. N-linked (GlcNAc. ..) (Pot. N-linked (GlcNAc. ..) (By N-linked (GlcNAc. ..) (By By similarity. By similarity.
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in Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: The soluble form (SDPP) derives from the membrane form (MDPP)
                                                                                                                                                                                                                                                                                                          Seidl R., Mann K., Schaeffer W.; "N-terminal amino-acid sequence of pig kidney dipeptidyl peptidase IV solubilized by autolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by proteolytic processing. SIMILARITY: Belongs to the peptidase 59B family. DPPIV subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a
                                                                                                                      TISSUE-Kidney;
PubMed-14719797; DOI=10.1515/BC.2003.172;
Baer J., Weber A., Hoffmann T., Stork J., Wermann M., Wagner L.,
Aust S., Gerhartz B., Demuth H.-U.;
"Characterisation of human dipeptidyl peptidase IV expressed in Fastoria Astructural and mechanistic comparison between the recombinant human and the purified porcine enzyme.";
Biol. Chem. 384:1553-1563(2003).
                                                                                                                                                                                                                     MEDLINE=94093209; PubMed=7903569;
Thomsen P.D., Gvist H., Marklund L., Andersson L., Sjostrom H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Assignment of the dipeptidylpeptidase IV (DPP4) gene to pig
                                                                                                                                                                                                                                                                                                                                     Biol. Chem. Hoppe-Seyler 372:213-214(1991).
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                                                                                                        [1]
NUCLEOTIDE SEQUENCE, AND FUNCTION.
                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
MEDLINE=91273813; PubMed=1675855;
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PIR; 147134; 147134.
PDB; 1CNV; X-ray; A/B/C/D=39-766.
PDB; 1CNW; X-ray; A/B/C/D=39-766.
SWR; P22411; 39-766.
                                                                                                                                                                                                                                                                 Mamm. Genome 4:604-607(1993).
                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 2-67.
                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE OF 38-71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soluble form.
                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                         chromosome 15g21
                                                                                                                                                                                                             TISSUE=Kidney;
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MEROPS; S09.003; -..

OR InterPro; IPR00137; Pept S9 AS.

DR InterPro; IPR00137; Peptidase_S9.

DR InterPro; IPR00137; Peptidase_S9.

InterPro; IPR003469; Peptidase_S9.

DR Pfan; PF00130; DPIVI N; I.

DR PROSTIE; PS00708; PRO ENDORED SER; 1.

PROSTIE; PS00708; PRO ENDORED SER; 1.

Mydrolase; Protease; Serine protease; Signal-anchor; Transmembrane.

PT CHAIN 38 766 Dipeptidase 4 membrane form.

CHAIN 1 766 Dipeptidase 4 membrane form.

Cycoplasmic (Potential).

To Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

Rarge relay system (By similarity).

"Arge relay system (By similarity).

"Arge relay system (By similarity).

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N-linked (GLGNAC...).
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88242 MW; 8800D520BAEA856D CRC64;
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   EYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF 732
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FBR-1990 (Rel. 14, Created)
01-FBR-2005 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 46, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
14-SEP-2005 (Rel. 48, Last annotation update)
15-SEP-2005 (Rel. 48, Last annotation update)
17-SEP-2005 (Rel. 48, Last annotation)
18-SEP-2005 (Rel. 46, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN SEQUENCE OF 28-58, AND TISSUE SPECIFICITY.

MEDILINE=90228995; PubMed=1970322;

MCGaughan G.W., Wickson J.B., Creswick P.P., Gorrell M.D.;

"Identification of the bile canalicular cell surface molecule GP110 as

the ectopoptidase dispetidyl peptidase IV: an analysis by tissue
distribution, purification and N-terminal amino acid sequence.";

Hepatology 11:534-64(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89123496; PubMed-2563382; Ogata S., Misumi Y., Ikehara Y.; "Primary structure of rat liver dipeptidyl peptidase IV deduced from its cDNA and identification of the NH2-terminal signal sequence as the
                                                                           DGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                               VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 281-302, AND MUTAGENESIS OF GLY-629; TRP-630; SER-631; TRY-632 AND GLY-633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hong W., Doyle D.; "CDNA cloning for a bile canaliculus domain-specific membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            studied by in vitro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein of rat hepatocytes.";
Proc. Natl. Acad. Sci. U.S.A. 84:7962-7966(1987)
                                                                                                                                                                                                                                                                                                                                                                                                           767 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 263:16892-16898(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane-anchoring domain.";
J. Biol. Chem. 264:3596-3601(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89034185; PubMed=3182821;
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                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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R GO; GO:0005625; C:soluble fraction; IDA.

R GO; GO:0004274; F:dippeptidy1-peptidase IV activity; TAS.

R GO; GO:0004274; F:dippeptidy1-peptidase IV activity; TAS.

R GO; GO:0004271; Peptidase IV and peptidolysis; TAS.

R InterPro; IPR001375; Peptidase S9.

R InterPro; IPR001375; Peptidase S9; I.

R Program; Pr001376; Peptidase S9; I.

R PR0517E; PS001706; PRO ENDER SRR; I.

R Aminopeptidase; Direct protein sequencing; Glycoprotein; Hydrolase; Maninopeptidase; Signal-anchor; Transmembrane.

R Protease; Serine protease; Signal-anchor; Transmembrane form.

T GHAIN 37 767 Dipeptidy1 peptidase 4 soluble form.

PT CHAIN 281 767 Dipeptidy1 peptidase 4 soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 624-648.

MEDLINE=92190188; PubMed=1347701;

Ggata S., Misumi Y., Tsuji E., Takami N., Oda K., Ikehara Y.;

"Identification of the active site residues in dipeptidyl peptidase IV by affinity labeling and site-directed mutagenesis.";

Blochemistry 31:2582-2587(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soluble form.
TISSUE SPECIFICITY: Expressed in bile ducts and other epithelial brush borders (small intestine, kidney, colon, pancreatic duct); acinar structures and alivary glands; endothelial structures and T cell areas in thymus, spleen and lymph node.

PTM: The soluble form (SDPP) derives from the membrane form (MDPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by proteolytic processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hong W., Doyle D., $^{\rm Hong \ W.}$ and a signal/anchor sequence of {\rm ^{\rm Holecular}} dissection of the NH2-terminal signal/anchor
                           Iwaki-Egawa S., Watanabe Y., Fujimoto Y.;
"N-terminal amino acid sequence of the 60-kDa protein of rat kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charge relay system (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR.
MEDLINE=90338089; PubMed=1974258; DOI=10.1083/jcb.111.2.323;
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Ensembl; ENSRNOG00000030763; Rattus norvegicus.
                                                                                                                           Hoppe-Seyler 374:973-975(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J02997; AAA41272.1; -; mRNA.
MEDLINE=94128239; PubMed=7905271;
                                                                                            dipeptidyl peptidase IV.
Biol. Chem. Hoppe-Seyler
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HSSP; P27487; 1PFQ.
SMR; P14740; 37-766.
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609 636 699 969 756

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A CERAINE-CS7BL/6J; PLOMPG-12466851; DOT-10.1038/nature01266;

MEDLINE-23154683; PubMed-12466851; DOT-10.1038/nature01266;

MEDLINE-23154683; PubMed-12466851; DOT-10.1038/nature01266;

MEDLINE-23154683; PubMed-12466851; DOT-10.1038/nature01266;

MIXAID I., OBACTO N., Saito R., Suzuki H., Sanonbach C., Gojobori T., Yagi K., Tomaru Y., Hall D.F., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Blake J.A., Pretcher C.F., Forrest A., Frazer K.S., A Gasterland T., Gariboldi M., Glesi C., Godzik A., Gough J., A Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D., A Kanaja A., Kawasawa Y., Kedrierski R.M., King B.L., Akanaja A., Kucchkini I.V., Lenhard B., Lyons B.L., Maxchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertes G., Pesole G.,
                                                                                                                                                                                                                                                 ASPDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYV
                                        ASFDGRGSGYQGDKIMHAINKRLGTLEVEDQIEAARQFLKMGFVDSKRVAIWGWSYGGYV
                                                                                                                                               TSWVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENF
                                                                                                               TSMVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENF
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
13-SEB-2005 (Rel. 48, Last sennotation update)
13-SEB-2005 (Rel. 48, Last annotation update)
Dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (T-cell activation antigen CD26) (Thymccyte-activating molecule)
(THAM) [Contains: Dipeptidyl peptidase 4 membrane form (Dipeptidyl peptidase IV membrane form); Dipeptidyl peptidase IV soluble form)
[Dipeptidyl peptidase IV soluble form)].

Musme-DD94; Synonyms-Cd26;

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=B10.A; TISSUE-Liver;
MEDLINE-55092780; PubMed=7999781;
Bernard A.-M., Mattei M.-G., Pierres M., Marguet D.;
"Structure of the mouse dipeptidyl peptidase IV (CD26) gene.";
Biochemistry 33:15204-15214(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule. A (CD26) included
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subgroup of serine proteases.";
J. Biol. Chem. 267:2200-2208(1992).
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STRAIN-Swiss; TISSUE-Thymus;
MEDLINE-92129288; PubMed=1370813;
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SHFLQQCFSL 766
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Submitted (SEP-1994)
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G-A: Reduced activity.
W->E: No effect on activity.
S->A: Reduced activity.
Y->F: No effect on activity.
Y->E: Reduced activity.
Y-\Li Reduced activity.
G->A: Reduced activity.
G->A: Reduced activity.
G->A: Reduced activity.
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L-> F (in Ref. 2).
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ive 53; Mismatches 56;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
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Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-20.

MEDLINES-91307787; PubMcd=1712807;
Vivier I., Marguet D.A., Gaquet P., Bonicel J., Black D., Li C.X.-Y.,

Bernard A.-M., Gorvel J.-P., Pierres M.;

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J. Immunol. 147:447-454(1991).
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                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                        Nature 420:563-573 (2002).
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
-!- FUNCTION: Removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the polypeptides residue is proline.
-!- CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Yaa-|-Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.
                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: The soluble form (SDPP) derives from the membrane form (MDPP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by proteolytic processing. SIMILARITY: Belongs to the peptidase S9B family. DPPIV subfamily.
                                                                                                                                                                                                                                                                                      SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Type II membrane protein. Also exists in a
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EMBL; U12629; AAA82213.1; -; Genomic DNA.
EMBL; U1259; AAA82213.1; JOINED; GENOMIC DNA.
EMBL; U12600; AAA82213.1; JOINED; GENOMIC DNA.
EMBL; U12601; AAA82213.1; JOINED; GENOMIC DNA.
EMBL; U12602; AAA82213.1; JOINED; GENOMIC DNA.
EMBL; U12603; AAA82213.1; JOINED; GENOMIC DNA.
                                                                                                                                                                                                                                                                                                                                                                                      soluble form.
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EMBL; AKOBS370; BARAZ183.1; -; mRNA.

EMBL; BC022183; AAH22183.1; -; mRNA.

EMBL; BC022183; AAH22183.1; -; mRNA.

SRR; P28843; 37-759.

SRR; P28843; 37-759.

MEROPS; S09.003; -.

RESEMBL; ENSWIGSG00000035000; Mus musculus.

MGI; MGI; MGI; 94919; Dpp4.

GO; GO:0016021; C:integral to membrane; TAS.

RO; GO:0046891; C:integral to membrane; TAS.

RICEPPO; IPR001375; Peptidase_S9.

InterPro; IPR001375; Peptidase_S9.

InterPro; IPR001375; Ser_estrs.

Refam; PR0032469; Peptidase_S9:

Refam; PR0031849; PRO ENDORPES SRR; 1.

RP031TE; PS00708; PRO ENDORPES SRR; 1.

Whinhopetidase; Direct protein sequencing; Glycoprotein; Hydrolase;

Whinhopetidase; Direct protein sequencing: Transmembrane.

WHALL PROSERTE; PRO ENDORPES SRR; 1.

CHAIN ADALAGA A membrane form
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Dipeptidyl peptidase 4 soluble form (By
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Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
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      EMBL, U12605; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12606; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12609; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12609; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12609; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12610; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12611; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12613; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12613; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12614; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12615; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12616; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12619; AAA82213.1; JOUNED; Genomic DNA.
EMBL, U12619; JAA82213.1; JOUNED; Genomic DNA.
EMBL, U12619; JAA82213.1; JOUNED; Genomic DNA.
EMBL, U12619; JAA82213.1; JOUNED; Genomic DNA.
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84.7%; Pred. No. 4.9e-222;
tive 57; Mismatches 50;
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Pfam; PP00930; DPPIV N; I.
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PEGHKLAYVWKNDIYVKVEPHLPSHRITSTGEENVIYNGITDWVYEERVFGAYSALWWSP
                                                                                                        253 VINATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN
                                                                                                                                                                                 CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNBEGYRHICYFQIDKKDCTFIT
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                                                                                                                                                                                                     CPSEQQHVEMSTTGWVGRFRPABPHFTSDGSSFYKIISDKDGYKHICHFPKDKKOCTFIT
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                                    NGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=259325;
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MUCLECTIDE SEQUENCE.

TISSUBA-Venom gland;

A Ogawa Y., Yanoshita R., Murayama N., Higuchi S., Samejima Y.;

L Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB158224; BAD06332.1; -; mRNA.

EMG.; A05.0004177; Framinopeptidase activity; IEA.

GO; GO:0004274; Frdipeptidayl-peptidase IV activity; IEA.

GO; GO:0004277; Framinopeptidase activity; IEA.

GO; GO:0006508; P:protelysis and peptidolysis; IEA.

GO; GO:0006508; P:protelysis and peptidolysis; IEA.

InterPro; IPR002471; Peptidase S9.

R InterPro; IPR002471; Peptidase S9.

R InterPro; IPR002469; Peptidase S9.
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Last sequence update)
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05-JUL-2004 (TrEMBLrel. 27, Last seque
05-JUL-2004 (TrEMBLrel. 27, Last annot
Dipeptidylpeptidase 4a (EC 3.4.14.5).
Name=DPPP4a;
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LOCCFSL 759
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                                                                                                   74 HSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLMKRQLITEERIPNNTQWVTWSP
                                                                                                                                                                                                         VGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEBVFSAYSALWWSPN
                                                                                                                                                                                                                                                                                                                             SPKNISBIVAPSSIISGDHYLSAVTWVTDERICVQWLRRIQNFSVLTICDY---SGAWHC
                                                                                                                                                                    TNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVMDICDYDESSGRWNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVARQHIBMSTTGWVGRFRPSEPHFTLDGNSFYKLISNBEGYRHICYFQIDKKDCTFITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPSKBAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDPIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 NETKFWYOMILPPHFDKSKKYPLLLDVYAGPCSOKADTVFRLNWATYLASTENIIVASFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCOYYSV
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                                                                              Gapa
                                                                              11;
                                                    DB 2; Length 751;
                                                62.7%; Score 2520.5; DB 2; Length larity 62.4%; Pred. No. 7.9e-163; Conservative 114; Mismatches 148; Indels
              Hydrolase; Transmembrane.
SEQUENCE 751 AA; 86127 MW; 6EA3F2D829BB97D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE 10

82 AGKHB

Q75882 AGKHB PRELIMINARY; PRT; 751 AA.

Q75882.

05-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Dipeptidalypeptidase 4b (EC 3.4.14.5).
ij
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733

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--HEATTAILSPDORFALLQYKYEKLWRHSYTASYHIYDFNTSSILDDALLPNDTQXISW 155
 PNGTFLAYAQFNDTEVPLIBYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 SVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRW 311
                                                                       38 SRSTYTLENYLNNDYVYKTHNLQWISGNQYLHETSNGNILRFDAETGTSSVVLLNTISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 FGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTW
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                                                     YLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHPI
                                                                                                                                                                                                                                                                            TRAINCAIDS SECURIORS,

A Piedlac B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,

A Piedlac P., Kuter S., Blagodatski A., Kostovska D., Koter M.,

A Piedlac P., Kuter S., Blagodatski A., Kostovska D., Koter M.,

Plachy J., Carninci P., Haysahizaki Y., Buerstedde J.M.;

T. Tenelunction analysis.",

Genome Biol. 6.R6(2005).

B. MEL, AJ720903; CAG32562.1; -; mRNA.

GO, GO:00104177; F:aminopeptidase activity; IEA.

GO; GO:0014177; F:aminopeptidase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:proteolylasis and peptidolysis; IEA.

R GO; GO:0016787; F:proteolylasis and peptidolysis; IEA.

InterPro; IPR00137; Peptidase_S9.

InterPro; IPR00137; Peptidase_S9.

InterPro; IPR00137; Ser estrs.

R Ffam; PF00136; Peptidase_S9.

InterPro; IPR00137; Ser estrs.

R PRGN; FROM SNDORPE SER; I.
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SEQUENCE 759 AA, 86343 MW, B9A0C38CCB8644AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.7%; Score 2519; DB 2;
64.7%; Pred. No. 1e-162;
ive 93; Mismatches 150;
                                                                                                                                                                                                                                                  759 AA
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                                                                                                                                                                                                                                                  CHICK PRELIMINARY;
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                                                                                                                            740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPKNISEIVAPSSIISGDHYLSVVTWVTDERICVQWLRRIQNFSVLTICDY---SGAWHC 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSSV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 TNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 LVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFITK 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 RKTYTLIDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GRFLAFAEINDTEVPVMEYSFYSEDTLQYPKTIKIPYPKAGAINFTIRLFVLDI----SL
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Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
brevicaudus).
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 751;
                                                                                                                                     NUCLEAURY SECRETARY

A GRAWA Y., Yanoshita R., Murayama N., Higuchi S., Samejima Y.;

C ILSSUE-Venom gland;

L Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

E SHBL; AB158225; BAD06333.1; -; mRNA.

R GO; GO:0004274; F:aminopeptidase activity; IEA.

R GO; GO:0004274; F:indropeptidase activity; IEA.

R GO; GO:0004274; F:indropeptidase activity; IEA.

R GO; GO:0004274; F:indrolase activity; IEA.

R GO; GO:0004274; F:indrolase activity; IEA.

R GO; GO:0004274; F:indrolase activity; IEA.

R GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.

R InterPro; IPR002469; Peptidase S9B.

R InterPro; IPR00340; Peptidase S9B.

R FRGMI; PF00930; DPPIV N; I.

R FRGMI; PF00187; PEDEC ENDOPEP SER; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              751 AA; 86155 MW; DAF219B4FEE7629A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.7%; Score 2519.5; DB 2;
Best Local Similarity 62.4%; Pred. No. 9.2e-163;
Matches 454; Conservative 114; Mismatches 148;
                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                             NCBI_TaxID=259325;
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  Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Youchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 RKTFTLEDYPSDBYRPKSFQLKWVSENEFVFRDKDNVLIFNVDNETTTEIISNTTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSIND--YSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SPVGHKLAYVWENNIYIKEVPGGISTTITTNGEHNKILNGIPDWVYEERMFSTNYALWWS
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TISSUE=Kidney;

Klein S., Gerhard D.S.;

Klein S., Gerhard D.S.;

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

B. Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

B. GO; GO:0004017; F: mambrane; IRA.

R. GO; GO:0004177; F: mamnopeptidase activity; IRA.

GO; GO:0004274; F: Hidpeptidyl-peptidase IV activity; IRA.

GO; GO:0004287; F: Prolyl oligopeptidase activity; IRA.

R. GO; GO:0004287; F: Prolyl oligopeptidase activity; IRA.

R. GO; GO:0006508; F: Prolyl oligopeptidase activity; IRA.

R. InterPro; IPR002469; Peptidase_S9.

R. InterPro; IPR002469; Peptidase_S9.

R. InterPro; IPR003175; Peptidase_S9.

R. Pfam; PR00330; DPPIV N; P.

R. PROSITE; PRO0326; Peptidase_S9; I.

R. PROSITE; PRO0326; Peptidase_S9; I.

R. PROSITE; PRO0326; PEPTIME SER; I.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                        TC--HRKNNFWKKVQLAGW--QISAICPLFAPDNTTYYKVFSNTEGYKHIHYINGTEAPV
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                                                                                                                                              369 TPITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVT-CLSCELNPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Kidney;
MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
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Last sequence update)
Last annotation update)
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NCBI_TaxID=8355;
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HMSHFIKQCFSLP 759
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Q641D6;
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Name=LOC397888;
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325 NCQPPVYKQ----SSTGWVGYFQPSAPYFTQDGLKYYKIISNKEGYKHIHLFE-GSKDPV 379
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QYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKL 488
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                             NCL -- VARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCT
                                                                                                                                                                                                                                                                                                                                                                                                                                   VASPDGRGSGYQGDXIMHAINRRLGTPEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGY
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                                                            SVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRW
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                                                                                                                                                                                                                                                                                                                                                                                 Wilson R.K.;
Submitted (ARR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; ACCOP7750; AAYS4205.1; -; Genomic_DNA.
GO; GO:0016020; C:membrane; IEA.
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o sapiens BAC clone RP11-576116.";
to the EMBL/GenBank/DDBJ databases.
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13-SEP-2005 (TrEMBLral. 31,
13-SEP-2005 (TrEMBLral. 31,
Hypothetical protein FAP.
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NUCLEOTIDE SEQUENCE.
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Submitted (JUN-1999)
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Submitted (OCT-1999)
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Submitted (OCT-2000)
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEOUENCE.
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NUCLEOTIDE SEQUENCE
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                                                                                                                                    671 QVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMMYTDEDHGIASSTAHQHIYTHMS
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                                                                                   SWVLGSGSGLFKCGIAVAPVSSWHYYDSIYTERYMGLPTPEDNLDNYLSSTVWARAQKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEFG
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     25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUR=Skin;
MEDLINE=97390076; PubMed=9249015;
Vlasak R., Vilas U., Strobl B., Kreil G.;
"CDDA cloning and expression of secreted Xenopus laevis dipeptidyl aminopeptidase IV.";
                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Dipeptidyl-peptidase IV (EC 3.4.14.5)
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 748;
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                                                                                                                                                                                                                                                                                                                                              748 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 247:107-113(1997)
EMBL; Y08932; CAA70136.1; -; mRNA.
HSSP; P27487; 1PFQ.
                                                                                                                                                                                                                                                                                                                                              P70092_XENLA PRELIMINARY;
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Best Local S:
Matches 430
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                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                               Length 760;
R GO; GO:0003824; F:catalytic activity; IEA.
R GO; GO:0004274; F:dipeptidyl-peptidase IV activity; IEA.
GO; GO:0004287; F:prolyl oligopeptidase activity; IEA.
R GO; GO:0006508; P:protolyl oligopeptidase activity; IEA.
R InterPro; IPR002471; Peptidase S9.
R InterPro; IPR001375; Peptidase S9.
R InterPro; IPR001375; Peptidase S9.
R InterPro; IPR001379; Peptidase S9.
R Pfam; PF00930; DPPIV N; I.
Pfam; PF00930; PROPIV N; I.
R PROSITE; PS00708; PRO ENDOPEP SER; I.
Hydrolase; Hypochetical protein; Transmembrane.
O SEQUENCE 760 AA; 87713 MW; 7PF817B5A4F75142 CRC64;
                                                                                                                                                                                                                                                                                                 Indela
                                                                                                                                                                                                                                                           Query Match 54.1%; Score 2175; DB 2; Best Local Similarity 52.6%; Pred. No. 2.7e-139; Matches 390; Conservative 139; Mismatches 198;
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RESULT 15 SEPR_HUMAN

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIBULINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,
And Stableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
And S.L., Doquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
And S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
And S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Anilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Anilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Kettemn M., Madan A., Rodriguez S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fibroblast,
MEDLINE=94261645; PubMed=7911242;
Scanlan M.J., Raj B.K.M., Calvo B., Garin-Chesa P., Sanz-Moncasi M.P.,
Healey J.H., Old L.J., Retign W.J.;
"Molecular cloning of fibroblast activation protein alpha, a member of
the serine procease family selectively expressed in stromal
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
Q12884; O00199; Q86229; Q99998; Q9UID4; 28-FRB-2003 (Rel. 41, Created) 28-FRB-2003 (Rel. 41, Last sequence update) 13-SFB-2005 (Rel. 44, Last annotation update) Seprase (Rcl. 43, Last annotation update) membrane serine protease) (170-kDa melanoma membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldstein L.A., Chen W.-T.;
"Identification of an alternatively spliced seprase mRNA that encodes a novel intracellular isoform.";
J. Blol. Chem. 275:2554-2559 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-97388251; PubMed-9247085; DOI=10.1016/S0925-4439(97)00032-X; Goldstein L.A., Ghersi G., Pineiro-Sanchez M.L., Salamone M., Yeh Y., Flessate D., Chen W.-T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flessate D., Chen W.-T.; "Molecular cloning of seprase: a serine integral membrane protease
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MEDLINE=20112818; PubMed=10644713; DOI=10.1074/jbc.275.4.2554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of the 170-kDa melanoma membrane-bound (seprase) as a serine integral membrane protease."; J. Biol. Chem. 272:7595-7601(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT THR-354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblasts of epithelial cancers.";
Proc. Natl. Acad. Sci. U.S.A. 91:5657-5661(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1361:11-19(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM 2).
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                                                          PROTEIN SEQUENCE OF 192-208; 220-240 AND 510-521.

MEDLINE=94327249; PubMed=7519584;

MEDLINE=94327249; PubMed=7519584;

Garlin-Chesa P., Healey J.H., Portunato S.R., Scanlan M.J., Raj B.K.M.,

Garlin-Chesa P., Healey J.H., Old L.J.;

"Fibroblast activation protein: purification, epitope mapping and induction by growth factors.";

Int. J. Cancer 58:385-392(1994).

Int. J. Cancer 58:385-392(1994).

Int. J. Cancer way have a role in tissue remodeling during development and wound healing, and may contribute to invasiveness in malignant
                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Degrades gelatin and heat-denatured type I and type IV collagen, but not native type IV or type IV collagen. Does not cleave laminin, fibronectin, fibrin or casein.

SUBUNIT: Homodimer, or heterodimer with DPP4. The monomer is
 Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                          Name=2; Synonymes5, Truncated, 1804-2; Synonymes5, Truncated, 1804-2; Synonymes5, Truncated, 1804-2; Sequence-VSP 005367; ISOUR SPECIFICITY: Fibroblast specific.
INDUCTION: In fibroblasts at times and sites of tissue remodeling during development, tissue repair, and carcinogenesis.
PTM: N-glycosylated.
FTM: The N-terminus may be blocked.
SIMILARITY: Belongs to the peptidase S9B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "..." (2010005887; C:integral to plasma membrane; TAS.

RGO; GO:0005887; C:lamellipodium; IDA.

RGO; GO:0004274; F:dipeptidyl-peptidase | NAS.

RGO; GO:0004274; F:metalloendopeptidase activity; NAS.

RGO; GO:0004203; F:metalloendopeptidase activity; TAS.

RGO; GO:0004203; F:protein homodimerization activity; NAS.

RO; GO:0004203; F:protein homodimerization activity; NAS.

RITEPTO: IPR002409; Peptidase S9.

INTERPTO: IPR002409; Peptidase S9.

INTERPTO: IPR003795; Ser_estrs.

R ATTACTOR PRO0370; Peptidase S9; I.

R PROSITE; PS00708; PRO ENDOREP SER; I.

R PROSITE; PS00708; PRO ENDOREP SER; I.

R JD-structure; Alternative splicing; Direct protein sequencing; W Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein. Found in cell surface lamellipodia, invadopodia and on shed vesicles.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=L;
IsoId=Q12884-1; Sequence=Displayed;
Note=Major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal-anchor for type II membrane protein (Potential).

Extracellular (Potential).

Charge relay system (By similarity).

Charge relay system (By similarity).

Charge relay system (By similarity).
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                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Ensembl; ENSG00000078098; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U09278; AAB49652.1; -; mRNA.
EMBL; U76333; AAC51668.1; -; mRNA.
EMBL; AF007822; AAF21600.1; -; mRNA.
EMBL; BC026250; AAF21650.1; -; mRNA.
PDB; 1268; X-ray; A=39-757, B=-.
MEROPS; S09.007; --
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les 389; Conservative 138; Mismatches 200; Indels
N-linked (GlCNAC. ..) (Potton-linked (GlCNAC. ..) (FTId=VAR. 019691. ...) (FTID=VAR. 0
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8.1e-139;
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

Run on:

February 15, 2006, 13:10:58; Search time 44 Seconds (without alignments) 1618.191 Million cell updates/sec

US-10-659-055-3 4020 Title: Perfect score:

1 ADPGGSHHHHHHHSRKTYTLT.....AHQHIYTHMSHFIKQCFSLP 740 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: pirl:* 2: pir2:* 3: pir2:* 4: pir4:* PIR 80:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	αı	Description
-	3933	97.8	992	-	CDHU26	dipeptidyl-peptida
7	3407.5	84.8	792	-	A39914	dipeptidyl-peptida
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4	1960.5	48.8	759	N	I38593	fibroblast activat
S	1129	28.1	803	N	168600	dipeptidyl aminope
9	1129	28.1	865	~	154331	
7	1106	27.5	803	~	A41793	
89	950.5	23.6	793	~	T41703	
O	914	22.7	818	ч	A30107	
10	799.5	19.9	711	~	866261	Ω
11	745.5	18.5	829	~	T19514	hypothetical prote
12	733	18.2	931	~	A49737	
13	725	18.0	799	~	T25174	hypothetical prote
14	720	17.9	779	N	T25173	hypothetical prote
15	628	15.6		7	A87516	(D)
16	594.5	14.8		~	JC5142	X-Pro dipeptidyl-p
17	590.5	14.7		~	T37700	probable dipeptidy
18	445.5	11.1	931	~	T32919	hypothetical prote
19	334.5	8.3		~	F82858	dipeptidyl-peptida
20	272	6.8		N	E70025	probable acylamino
21	244.5	6.1		N	JC8016	acylaminoacyl-pept
22	226	5.6		N	F71174	hypothetical profe
23	221	5.5		~	H72474	probable acylamino
24	219	5.4	642	~	C71137	hypothetical prote
25	214	5.3		~	E75057	peptidase PAB1418
26	205	5.1		~	H75007	probable acylamino
27	205	5.1		~	E87495	prolyl oligopeptid
28	191	4.8	709	~	B82580	ij
53	188	4.7		~	F72568	

on in a land on a	propante acytamino	prolyl oligopeptid	acylamino-acid-rel	conserved hypothet	prolyl oligopeptid	F44B9.1 protein -	acylaminoacyl-pept	oliqopeptidase B (hypothetical prote	probable peptide h	probable acylamino	probable acylamino	hypothetical prote	acylaminoacyl-pept	dipeptidyl-peptida	acylaminoacyl-pept
10000	7000	5/5/80	C97775	B87580	D87651	S44807	B84381	AB0217	875772	T35378	D72636	F72455	F84199	S07624	S14746	P90299
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	1	7/2	174	173.5	168	163.5	156.5	154.5	154	153.5	149	147.5	147	146.5	145	143
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RESULT 1

dipeptidyl-peptidase IV (EC 3.4.14.5) - human
NyAlternate names: cell surface glycoprotein CD26; thymocyte-activating molecule (THAM)
Syspecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Bloc-1993 #sequence revision 23-Aug-1996 #text change 09-Jul-2004
C;Accession: S24313; B42408; Ā42408; B61136; S59510; I56154; S59857; S15520
R;Misumi, Y.; Hayashi, Y.; Arakawa, F.; Ikehara, Y.
Biochim. Blophys. Acta 1131, 333-336, 1992
A;Title: Molecular cloning and sequence analysis of human dipeptidyl peptidase IV, a sf
A;Reference number: S24313; MUID:92329551; PMID:1352704

A; Receasion: S4431 A; Receasion: S4431 A; Receasion: S4531 A; Receasion: S4531 A; Residues: 1-6, T., 8-766 A; Ritle: Dipeptidy! Peptidase IV (CD 26) gene expression in enterocyte-like colon cancoming in the colon cancoming in cancoming in the colon cancoming in the col

A; Accession: S59510

A Molecule type: DNA A;Residues: 1-31 & BORS. A;Cross-rences: UNIPARC:UPI000016B4A6; GB:S79876; NID:g1195574; PIDN:AAB35614.1; PI R;Tanaka, T.; Camerini, D.; Seed, B.; Torimoto, Y.; Dang, N.H.; Kameoka, J.; Dahlberg, J. Immunol. 149, 481-486, 1992 A;Title: Cloning and functional expression of the T cell activation antigen CD26. A;Reference number: 156154; MUID:92325476; PMID:1352530

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A,Accession: A31781
A,Molecule type: mRNA
A,Residues: 1-40 <403 >
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A,Residues: 281-302 - KWA>
A,Cross-references: UNIPARC:UP10000172A3A
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A;Status: translated from GB/EMBL/DDBJ
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R;Abbott, C.A.; Baker, E.; Sutherland, G.R.; McCaughan, G.W.
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A;Reference number: S59857; MUID:95012454; PMID:7927537
A;AClecule type: DNA
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A;Introns: 2/3; 32/1; 65/1; 95/3; 122/3; 140/2; 164/3; 205/1; 258/3; 296/2; 341/3; 356/3
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A;Map position: 2q24.3-2q4.3
A;Introns: 2/3; 32/1; 65/1; 95/3; 122/3; 140/2; 164/3; 205/1; 258/3; 296/2; 341/3; 356/3
A;Map position: 2q24.3-2q4.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 GHSINDYSISPDGGFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTWS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLIDYTKVTCLSCELNPERCQYYS 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 VINATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEBGYRHICYPQIDKKDCTFIT 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
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Pred. No. 6.5e-259;
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A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-792 < HON3
A; Cross-references: UNIPROT: P14740; UNIPARC: UP1000017098A; GB: U02997; NID: G204463; PIDN: R; Ogata, S.; Misumi, Y.; Ikehara, Y.
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A; Accession: A33315
A; Molecule type: mRNA
A; Mo
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A;Cross-references: UNIPARC:UP10000172A2B; UNIPARC:UP10000172A30; UNIPARC:UP10000172A31;
A36; UNIPARC:UP10000172A37
A;A;Casughan, G.W.; Mickson, J.B.; Creswick, P.F.; Gorrell, M.D.
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A;Title: Identification of the bile canalicular cell surface molecule GP110 as the ectop
quence.
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A;Cross-references: UNIPARC:UPI0000172A38
B;Ogata, S.; Misumi, Y.; Tsuji, E.; Takami, N.; Oda, K.; Ikehara, Y.
B;Ogata, S.; Misumi, Y.; Tsuji, E.; Takami, N.; Oda, K.; Ikehara, Y.
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A;Molecule type: protein
A;Molecule type: protein protein
A;Molecule type: protein protein of rat kidney dipeptidyl patid: Chem. Hoppe-Seyler 374, 973-975, 1993
A;Reference number: S38949; MUID:94128239; PMID:7905271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dipeptidyl-peptidase IV (EC 3.4.14.5), membrane-bound form precursor - rat
NyAlternate names: GP110; membrane glycoprotein 110K; OX-61
NyContains: dipeptidyl-peptidase IV, soluble form
Cispecies: Rattus norvegicus (Norway rat)
Cjate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
CjAccession: A39914; A33315; B33315; A60730; A42203; S38949; A31781
RiHong, W.; Doyle, D.
Proc. Natl. Acad. Sci. U.S.A. 84, 7962-7966, 1987
A;Title: cDNA cloning for a bile canaliculus domain-specific membrane glycoprotein of
A;Reference number: A39914; MUID:88068516; PMID:3479775
732
                                                                               R.Hong, W.; Doyle, D. 1692-16998, 1988
J. Biol. Chem. 263, 1692-16998, 1988
A;Title: Membrane orientation of rat gpl10 as studied by in vitro translation.
A;Reference number: A31781; MUID:89034185; PMID:3182821
EYLLIHGTADDNVHPQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF
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    Comment: This protein is localized to the bile canaliculus, which is the apical domain
C;Comment: This protein is localized to the bile canaliculus, which is the apical dom C;Superfamily: dipeptidy-peptidase IV
C;Superfamily: dipeptidyl-peptidase IV
C;Reywords: dipeptidyl-peptidase, membrane-bound form #status experimental cNATW
F;1-28/Domain: signal sequence #link MATS #status experimental cSIG>
F;1-28/Domain: intracallular #status predicted cINT>
F;7-28/Domain: intracallular #status predicted cINT>
F;2-34/Domain: extracellular #status predicted cXT>
F;2-34/Domain: propeptide #link MATS #status experimental cPRO>
F;2-34/Domain: propeptide #link MATS #status experimental cPRO>
F;3-732/Pordouct: dipeptidyl-peptidase, soluble form #status experimental cNATS>
F;81-792/Pordouct: dipeptidyl-peptidase, soluble form #status experimental covalent) #status |
F;81-702/Active site: Ser #status experimental
F;709,741/Active site: Asp, His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                        CPTTQEHIETSATGWVGRFRPAEPHFTSDGSSFYKIVSDKDGYKHICQFQKDRKPEQDCT
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                                                                                                                                                                                84.8%; Score 3407.5; DB 1; Length 792;
84.5%; Pred. No. 3.2e-223;
tive 54; Mismatches 56; Indels 3;
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dipeptidyl-peptidae IV (EC 3.4.14.5) alpha chain - mouse
Nylterater names: CD26 alpha subunit; TRAM alpha subunit
C;Species; Nus muscrilus (house anouse)
C;Dectes; D; Bernard, A.M.; Vivier, I.; Darmoul, D.; Naquet, P.; Pierres, M.
J; Nocesion: S23722, NulD: S210288; PMID: 1370813
A;Recesion: S23722, NulD: S210288; PMID: 1370813
A;Recesion: S23724
A;Recesion: S23724
A;Recesion: S23725, NulD: S210288; PMID: 1370813
A;Recesion: Rédés
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84.2%; Score 3386; DB 1;
Best Local Similarity 84.6%; Pred. No. 8.6e-222;
Matches 615; Conservative 57; Mismatches 51;
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dipopuldyl aminopeptidase like protein - human

Gispecies: Homo sapiens (man)

Cispecies: Homo sapiens (man)

Cispecies: Homo sapiens (man)

Cispecies: No6-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

Cispecies: No7-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

Rivokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.

Hum. Mol. Genet. 2, 1037-1039, 1993

A;Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-relat

A; Reference number: I54331; MUID:93372805; PMID:8103397

A; Accession: 168600

A; Status: preliminary; translated from GB/EMBL/DDBJ
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184 GWGPKGQQLIPIPENNIYYCAHVGKQAIRVVSTGKEGVIYNGLSDWLYEEBILKTHIAHW
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                                                                              AIWGWSYG-GYVT-----SMVLGSGSGVPKCGIAVAPVSRWEYYDSVYTERYMGLP
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                                                                                                                                      LSCELNPERCOYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKML
                                                                                                                                                                                                               QNVQMPSKXLDF11LNETKFWYQM1LPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWA
                                                                                                                                                                                                                                                                                        TYLASTENIIVASFDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRI
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                                                           360 YPQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDY-TKVTC
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Best Local Similarity 32.7%; Pred. No. 1.4e-68;
Matches 244; Conservative 155; Mismatches 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTDEDHGIASSTAHQHIYTHMSHFIKQCFSL 739
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NiAlternate names: FAP-alpha
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: 138593
R;Scanlan, M.J; Raj, B.; Calvo, B.; Garin-Chesa, P.; Sanz-Moncasi, M.P.; Healey, J.; Ol
R;Scanlan, M.J; Raj, B.; Calvo, B.; Garin-Chesa, P.; Sanz-Moncasi, M.P.; Healey, J.; Ol
R;Scanlan, M.J; Raj, B.; Calvo, B.; Garin-Chesa, P.; Sanz-Moncasi, M.P.; Healey, J.; Ol
A;Reference number: 138593
A;Reference number: 138593
A;Recession: 138593
A;Revel manary
A;Molecule type: mRNA
A;Reaidues: 1-759 < RES
A;Conserreferences: UNIPARC:UPIO000175B7D; EMBL:U09278; NID:g507749; PID:g507750
C;Genetics: 1-759 < RES
A;Conserreferences: CDB:374184; OMIM:600403
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204 EMLPTKYALWASPNGKFLAYAEFNDKDIPVIAYSYYGDE--QYPRTINIPYPKAGAKNPV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 VKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVM 299
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                                                                                  552
                                                                                                                                                           612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLLIHGTADDNVHPQQSAQISKALVDVGVDPQAMWYTDEDHGIASSTAHQHIYTHMSHF 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VFLENSTFDEFGHSIN--DYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITE 119
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                           VSPSKEAKYYQLGCWGPGLPLYTLHRSTDHKELRVLEDNSALDRHLQDVQMPSKKLDFIV
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                                                                                                                                                                                                                                                      LNETKFWYQMILPPHPDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
                                                                                                                                                           DGRGSGYQGDKIMHAINRRLGIFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references: GDB:374184; OMIM:600403
A;Map position: 243-2423
C;Superially: dipeptidyl-peptidase IV
C;Keywords: transmembrane protein
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LQQCFSL 759
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310 RWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYF	RESULT 7 A41793 dipeptidy1 aminopeptidase-like protein (EC 3.4.14) short form, DPPX-S - bovine C; Species: Bos primigenius taurus (cattle) C; Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: A41793 R; Mada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R.J.; Shimasaki, S. Proc. Natl. Acad. Sci. U.S.A. 89, 197-201, 1992 A; Title: Differential expression of two distinct forms of mRNA encoding members of a d; ARCESSION: A41793 A; Reference number: A41793; MUID:92108018; PMID:1729689 A; Accession: A41793 A; Residues: preliminary; not compared with conceptual translation A; Rosidues: Le03 c/MAD> A; Residues: Le03 c/MAD> A; Residues: Leose extracted from NCB1 backbone (NCBIP:75138) C; Superfamily: dipeptidyl-peptidae lunipeptide hydrolase; glycoprotein C; Keywords: dipeptidyl-peptide hydrolase; glycoprotein F; 257,342/Binding site: carbohydrate (Asn) (covalent) #status predicted	Query Match 27.5%; Score 1106; DB 2; Length 803; Best Local Similarity 32.4%; Pred. No. 5.1e-67; Matches 242; Conservative 158; Mismatches 300; Indels 48; Gaps 22;	Qy 14 RKTYTLTDYLKNTYRLKLYSLRWISDHBYLYK-QBNNILVPNAEYGNSSVFLENSTFDEF 72	Qy 73 GHSINDYSISEDGQFILLEXNYVKQWRHSYTASYDIYDLNKRQLITEERIFN-NTQWV 129 1	Qy 130 TWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVXEBEVFSAVSALW 189	Qy 190 WSPNGTFLAXAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNFTVKFFVNYTDS 249
0y 310 RWNCLVARQHIEMSTTGRVGREPEBEPHTLDGNSFYKIISNBEGTRHICYF	RESULT 6 154331 dispetidyl aminopeptidase like protein - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 C;Accession: I54331 R;Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K. R;Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K. Hum. Mol. Genet. 2, 1037-1039, 1993 A;Title: Non-conservation of a catalytic residue in a dipeptidyl aminopeptidase IV-relat A;Reference number: I54331; MUID:99372805; PMID:8103397 A;Accession: I54331 A;Accession: I54331 A;Accession: I54331 A;Accession: I54331 A;Accession: I54331 A;Cross-references: UNIPROT:P42658; UNIPARC:UPI0000047378; GB:M96859; NID:g306705; PIDN: C;Superfamily: dipeptidyl-peptidase IV C;Superfamily: dipeptidyl-peptidase IV C;Superfamily: dipeptidyl-peptidase IV Best Local Similarity 32.7%; Pred. No. 1.6e-68; Matches 244; Conservative 155; Mismatches 303; Indels 44; Gaps 20;	OY 14 RKTYTLIDYLKOYTYRLKLYSLRWISDHBYLYK-OENNILVFNAEYGNSSVFLENSTFDEF 72 	Qy 73 GHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPN-NTQWV 129	Qy 130 TWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEEVFSAYSALM 189	QY 190 WSPNGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVNNTDS 249	QY 250 LSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVMDICDYDESSG 309 DD 361 LNGPTHDLEMMPPDDPRMREYYITMVKWATSTKVAVTWLNRAQNVSILTLCDATTG 416

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submitted to the EMBL Data Library, June 1994
A; Reference number: $46773
A; Reference number: $46773
A; Accession: $46773
A; Accession: $46770
A; Roberts, C.J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.
B; Roberts, C.J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.
A; Title: Structure, biosynchesis, and localization of dipeptidyl aminopeptidase B, an i., A; Accession: A30107
A; Reference number: A30107; MUID:89174971; PMID:2647766
A; Accession: A30107
A; Residues: 1-82,'H', 84-124,'N', 126-181,'LRRLET', 189-199,'N', 201-365,'DFKRGKERKF', 376-5,'A; A; Accessiones: UNIPARC:UPI0000172A3C; EMBL:X15484
A; A; Accession: As a Asn
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S.Superfamally: dipoptidyl-peptidase IV
C;Keywords: dipoptidylpeptide hydrolase; glycoprotein; transmembrane protein; yeast vac
F;30-45/Domain: transmembrane #status predicted <TMM>
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232
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                                                                                                               282 PGNPNPSVSLFV--ADLNSNASSNPSLWHNEP----LAEPVVQNVLWVNTSSVLVQFTNR
                                                                                                                                                                                                                                                                                                                                                                                                                             AGAVNPTVKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRR
                                                                                                                                                           293 IQNYSVMDICDYDESSGRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLD-----GNS
                                                                                                                                                                                                   NSTCITARLLDTELKS-----IHTVKTECLEEGWY-EVOOSAKMFPLNNSLVWENWSDG
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  -SLQYPKTVRVPYPK
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A,Crose-references: SGD:S0001070; MIPS:YHR028c
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41703
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
R;Murphy, L.; Harris, Data Library, August 1998
A;Reference number: Z22011
A;Accession: T4103
A;Reference number: Z22011
A;Molecule type: DNA
A;Residues: 1-793 <MUR>
A;Residues: 1-793 <MUR>
A;Residues: 1-793 <MUR>
A;Residues: 1-793 <MUR>
A;Constimental source: strain 972h-; cosmid c2Ell -chimeric
C;Genetics:
A;Gene: SPACZEll.08
A;Map position: 1
C;Superfamily: dipeptidyl-peptidase IV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NTOW----VTWSPVGHKLAYVWNNDIYV-KIEPNLPSYRITWTGKEDIIYNGITDWYYB 178
                                                                                 361
                                                                                                         355 ----VCTKKH-EDESEAMLHR-QNEEPVFSKDGRKFFFVRAIPQGGGKFYHITVSSSQP 408
                                                                                                                                                                                        583
                                                                                                                                                                                                                                                                                                                                                                                                                                  PDEFGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPN---- 124
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                           362 QIDKKDCTFITKGTWEVIGIEALTSD----YLYYISNEYKGMPGGRNLYKIQLSDYTKVT 417
                                                                                                                                                                                                                                               CLSCEINPERCOYYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKM 477
                                                                                                                                                                                                                                                                    478 LONVOMPSKKLDFIILNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNW 537
                                                                                                                                                                                                                                                                                                                                                                                                          538 ATYLASTENIIVASFDGRGSGYOGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKR 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAIWGWSYGGYVTSMVL---GSGSG-VFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDH--YRNSTVMSRAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTD 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
  LSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSG
                                                                                                                                                                                                                                                                                                                                                      14 RKTYTLTDYLKNTYRLKLYSLRWISDH----EYLYKQENNILVFNAEYGNSSVF-LENST
                                                                                 RWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEG----YRHICYF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDHGIASSTAHQHIYTHMSHFIKQCFSL 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | :|: | |:: : :| :| :| ESHYFSSAALQQHLHRSILGPFVECFRI 787
                                                                                    310
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-711 <KBA.
A;Residues: 1-711 <KBA.
C;Superfamily: dipeptidyl-peptidase IV
C;Keywords: dipeptidyl-peptidase IV
C;Keywords: dipeptidylpeptide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 IVD---GSFQGYTFSNDESKILLQKSSQSIYRHSFLGKFEVKDLKSRTVVS----LNNAN 125
                                                                                                                                                                                                                                                                                                                                                                                                                            68 TPDBFGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEBRIPNNTQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTWAT -- QERISLQWLRRIQNYSVMDIC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D------YDESSGRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYTKVTCLSCEL--NPERCQYY----SVSFSKEAKYYQLRCSGPGLPLYTLHSSVND 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C27C12.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 115-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accesion: T19514 R;Thomas, K. submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WV---TWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYBEEVPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TAYLYQLSSGKSAQLINFGSS----EKYYIPQLPQTNANDEIVVATANRHQN--KVDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 KVNTKTAAVSKLFTETDNAW---IETDNITME-------FLDDNSFL-WASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       352 BEGYRHICYPQIDKKDCTFITKGTWEVIGIEALTSDYLYYISNRYKGMPGGRNLYKIQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGLRVLEDNSALDKMLQNVQMPSKKLDFIIL-----NETKFWYQMILPPHFDKSKKYPLL
                                                                                                                                                                                                                                                                                                                       10 HHHSRKTYTLTDYLKONTYRLK-LYSLRWISDHE-YLYKQENNILVFNABYGNSSVFLENS
                                                                                                                                                                                                                                                                                                                                                                     17 HGLSAQEITLDKIYSGQYRAKGISGIASLNDGENYATIEPTGI----AKYSYKTSQKEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 YSALWWSPNGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : : | | : : | | EKGSINKVVSKINISTAKVPTKYILKDANG
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                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                      711;
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19.9%; Score 799.5; DB 2;
Best Local Similarity 29.9%; Pred. No. 2.7e-46;
Matches 227; Conservative 131; Mismatches 298;
          Accession: S66261
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X-Pro dipeptidyl-peptidase (BC 3.4.14.11) - Flavobacterium meningosepticum
X-Pro dipeptidyl-peptidase (BC 3.4.14.11) - Flavobacterium meningosepticum
C;Species: Plavobacterium meningosepticum
C;Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66561
B;Kabashima, T.; Yoshida, T.; Ito, K.; Yoshimoto, T.
Arch. Biochem. Biophys: 320, 123-128, 1995
A;Title: Cloning, sequencing, and expression of the dipeptidyl peptidase IV gene from A;Reference number: S66261; MUID:95314307; PMID:7793970
        predicted
                                                                                                                                                                                        50 HHSNTPDYQEPNSNYTNDGKLKVSFSVVRNNTFQPKYHBLQWISDN----KIBSNDLGLY 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWGNGNVLVKTTDRSSDILTVFLIDTIAKTSN----VVRN--ESSNGGWWEITHNTLFI 389
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                                                                                                                                                                                                                                                                    66
F;63,79,110,139,392,421/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                  223 VINDGSSFLFNGKPDMVYEEVFEDDKAAWWSPIGDYLAFLKIDESEVGEFIIPY-YVOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWTGKEDIIYNGITDWVYEEEVFSAYSALWWSPNGTFLAYAQFNDTEVP--LIEYSFYSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 NETKFWYQM-----ILPPHFDK--SKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ------VFNAEYGNS--SVFLENSTFDEFGHSINDYSI--SPDGQFILLEYNYVKOWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BSLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDV
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                                                                                                                                                          HHS-----RKTYTLTDYLK-----NTYRLKLYSLRWISDHEYLYKQENNIL---
                                                                                                            Gaps
                                                   ch 22.7%; Score 914; DB 1; Length 818; Il Similarity 32.3%; Pred. No. 5.7e-54; 258; Conservative 119; Mismatches 314; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HNANVIVFDKLLDWAKRAF 812
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Best Local S:
Matches 258
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aminopeptidase

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A;Cross-references: UNIPARC:UP10000136060; EMBL:L21944; NID:g347196; PIDN:AAA35119.1; PI R;Galisson, F.; Dujon, B. submitted to the EMBL Data Library, October 1995 A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosom A;Reference number: $60938 A;Accession: $60946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIPARC:UPI0000136060; GB:L21944; NID:g347196; PIDN
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A; Molecule type: DNA
A; Residues: 1-931 «GAL».
A; Residues: 1-931 «GAL».
A; Cross-references: UNIPARC: UPI0000136060; EMBL: X92441; NID: 91050762; PIDN: CAA63182.1;
A; Cross-references: UNIPARC: UPI0000136060; EMBL: X92441; NID: 91050762; PIDN: CAA63182.1;
B; Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, Bubmitted to the Protein Sequence Database, July 1996
A; Reference number: S67104
A; Accession: S67112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ajeccesario type: DNA

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A,Residues: 1-931 «GAM»
A,Cross-references: UNIPARC:UPI0000136060; EMBL:X92441; NID:91050762; PIDN:CAA63182.1;
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Galisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
A;Reference number: S71713; MUID:96437977; PMID:8840505
                                                                                                           dipeptidyl aminopeptidase (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein 05045; protein YOR219c; protein YOR50-9
C; Species: Saccharomyces cerevisiae
C; Date: 03-Mar-1994 #sequence revisiae
C; Date: 03-Mar-1994 #sequence Database, July 1993
R; Santa Anna-A, S.; Herskowitz, I.
R; Santa Anna-A, S.; Herskowitz, I.
A; Molecule type: DNA
A; McGession: A49737
A; Molecule type: DNA
A; Residues: 1-931 < SAN>
A; McGidues: 1-931 < SAN>
A; Cross-references: UNIFROT: P33894; UNIPARC: UP10000136060; GB: L21944; NID: G34719
R; Anna-Arriola, S.S.; Herskowitz, I.
Yeast 10, 801-810, 1994
A; Title: Isolation and DNA sequence of the STE13 gene encoding dipeptidyl aminop
A; Argeference number: S45451; MUID: 95066382; PMID: 7975897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 LNK---RQLITEERIPNNTQ------WVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRIT 160
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A.pescription: involved in processing of alpha-factor prepropheromone
A.pescription: dipeptidylpeptide hydrolase; glycoprotein; transmembrane protein
F.113-150/Domain: transmembrane #status predicted <TWM>
F.113-150/Domain: cransmembrane (Asn) (covalent) #status predicted
F.377/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.785,863,896/Active site: Ser, Asp, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 RKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENN--ILVFNABYGNSSVFLENSTFDE
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A;Cross-references: SGD:S0005745; MIPS:YOR219c
A;Map position: 15R
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A; Residues: 1-931 < ANN>
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                                   A;Accession: T19514
A;Accession: T19514
A;Geatus: preliminary; translated from GB/EMBL/DDBJ
A;Geatus: preliminary; translated from GB/EMBL/DDBJ
A;Geatus: DNA
A;Residues: 1-829 <WIL>
A;Cross-references: UNIPROT:Q18253; UNIPARC:UP1000007DC53; EMBL:Z69883; PIDN:CAA93743.1;
A;Restimental source: clone C27C12
C;Genetics: CSP:C27C12.7
A;Map position: X
A;Map position: X
A;Matrons: 4/3; 51/1; 123/3; 166/3; 188/2; 279/2; 392/3; 501/3; 553/1; 583/1; 606/2; 647
C;Superfamily: dipeptidyl-peptidase IV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 DWVYEEEVFSAYSALWWSPNGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKA 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 LIDYLKNIYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEFGHSIND 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.5%; Score 745.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 1.6e-42;
Matches 230; Conservative 128; Mismatches 283;
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A; Reference number: Z19134
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hypothetical protein T23F1.7a - Caenorhabditis elegans
C;Species: Caenorhabditis
R;Wilkinson, J.
R;Wilkinson, J.
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R;Wilkinson, J.
A;Reference number: Z1990
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A;Residues: 1-779 < WIL>
A;Residues: 1-779 < WIL>
C;Generice: Clone T23F1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                        352
                                                                                                                                                                                                                                                                                                                                                                                                        392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 LPLYTLHSSV-----NDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKR-----W 499
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                                                                                                                                 TOWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEVFSAY
                                                                                                                                                          185 IQAFKWNGKFNDFVFVESNKIYYQSSPEEGGLTRVSNGGEHTV-DGLFDWIYEERIFGRK
                                                                                                                                                                                                     SALWWSPNGTFLAYAQFNDTEVPLIEYSFYS-----DESLQYPKTVRVPYPKAGAVNP
                                                                                                                                                                                                                           244 DAMWWSTKGDQLAYASYDNHLTKNVSLKTYHRLBPYPIDTNFHYPKTF-----AKVLP
                                                                                                                                                                                                                                                                                      TY-----TLSIWNKKTEQSRQLDVQLKDSLSYHYLLAVKWLEINGTEQLVSV-WTNRYQ
                                                                                                                                                                                                                                                                                                                                       NYSVMDICDYDESSGRWNCLVARQHIE--MSTTGWVGRFRPSEPHFTLDGNSFYKIISNE
                                                                                                                                                                                                                                                                                                                                                           500 YOMILPPHF---DKSKKYPLLLDVYAGPCSOKADTVFRLNWATYLASTENIIVASFDGRG
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                                                                   NSTFDEFGHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNN
                                                                                                                                                                                                                                                                     TVKPFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTW----ATQERISLOWLRRIQ
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                         SGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKM--GFVDNKRIAIWGWSYGGYVT-SMV
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25174
R;Wilkinson, J.
R;Wilkinson, J.
A;Reference number: Z1999
A;Accession: T25174
A;Accession: T25174
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A;Accession: T25174
A;Catus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T25174
A;Catus: DNA
A;Catus: DNA
A;Catus: DNA
A;Catus: Caenores: UNIPROT:O18119; UNIPARC:UPI000061190; EMBL:Z81129; PIDN:CAB03412.1;
A;Caenores: Caenores: Clone T23F1
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| | :: |: |: :: |: :: | 216 INTGNIEPILPEKSDDNYELGLSKLSYAHFSPAYNYIYFVYENNLFLQQVNSGVAKKVT 335
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                                                                                                                                                                                    TQERISLQWLRRIQNYSVMDICDYDESSGRWNCLVARQHIEMSTTGWVGRFR-----PSE 335
                                                                                                                                                                                                       SPDTFREEITDR--NSKILDVKVYDIPSSQ--MLTVRNTNSNLFNGWIEKTKDILSIPPK 501
                                                                                                                                                                                                                                                    PHFTLDGNSFYKIISNEEGYRHICYP-QIDKKDCTFITKGTWEV----IGIEALTSDYL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG-VFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQVEYL- 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LIHGTADDNVHFQQSAQISKALVDVGV-DFQAMMYTDEDHGIASSTAHQHIYTHMSH 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Gene: CESP:T23F1.7b
:Map position: 5
:Introns: 13/3; 52/1; 111/3; 197/3; 366/3; 524/1; 557/1; 648/2; 703/1; 743/1
;Superfamily: dipeptidyl-peptidase IV
                                                                                                                                                                                                                                                                                                                                       161 WICKEDIIYNGIIDWVYEEEVFSAYSALWWSPNGTFLAYAQFNDTEVPLIRYSFYSDESL
                                                                                                                                                                                                                                                                                                                                                                                    PGLPLYTLH-----SSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNE-TKFW
                                                                                                                                                                                                                                                                                 502 PELKRMDYGYIDIHADSRGFSHLFYYPTVFAKEPIQLTKGNWEVTGNGIVGYEYET-DTI
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18.0%; Score 725; DB 2; Length 799;
Best Local Similarity 27.4%; Pred. No. 3.7e-41;
Matches 215; Conservative 119; Mismatches 282; Indels 168;
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87516
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
          A;Map position: 5
A;Introns: 13/3; 52/1; 111/3; 151/2; 177/3; 346/3; 504/1; 537/1; 628/2; 683/1; 723/1
C;Superfamily: dipeptidyl-peptidase IV
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                                                                                                                                                        SINDYSISPDGQ---FILLEYN------YVKQWRHSYTASYDIYDLNKRQLITE 119
                                                                                                                                                                      120 ERIPNNTOWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEE 179
                                                                                                                                                                                                                                                       EVFSAYSALWWSPNGTFLAYAQFNDTEVPLIEYSFYS-----DESLQYPKTVRVPYPK 232
                                                                                                                                                                                                                                                                                                       233 AGAVNPTVKPPVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTW----ATQERISLQ 288
                                                                                                                                                                                                                                                                                                                              -AKVLPTY-----TLSIWNKKTEQSRQLDVQLKDSLSYHYLLAVKWLBINGTEQLVSV- 323
                                                                                                                                                                                                                                                                                                                                                                                                      KIISNEEGYRHICYFQI--DKKDCT-------FITKGTWEVIGIEALTS 386
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                                                                                                      26 TYRLKLYSLRWISDHEYLYKQ----ENNILVFNA-----EYGNSSVFLENSTFDEFGH
                                                                                 Gaps
                                                       Query Match 17.9%; Score 720; DB 2; Length 779; Best Local Similarity 27.6%; Pred. No. 7.7e-41; Matches 218; Conservative 124; Mismatches 296; Indels 152;
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CESP: T23F1.7a
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B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Froc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter creacentus.
A.Recensce number: A87249; MUID:21173698; PMID:11259647
A.Accession: A87516
A.Accession: A87516
A.Residues: preliminary
A.Moclecule type: DNA
A.Residues: 1-738 <STO>
A.Accession: Calcology Complete Com
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ORGANISM: Homo sapiens
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US-10-522-789-2
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Sequence 7, Appli
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Sequence 12, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1192, Appl
Sequence 1192, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 21, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 35, Appli
                                                                   February 15, 2006, 13:26:39; Search time 18 Seconds (without alignments) 584.259 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
2: /cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
3: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
4: /cgn2 6/ptodata/2/pubpaa/PCT NEW FUB.pep:*
5: /cgn2 6/ptodata/2/pubpaa/US10 NEW FUB.pep:*
6: /cgn2 6/ptodata/2/pubpaa/US10 NEW FUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/US10 NEW FUB.pep:*
8: /cgn2 6/ptodata/2/pubpaa/US11 NEW FUB.pep:*
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Biocceleration Ltd.
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US-11-116-939-13
US-11-116-931-13
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US-11-176-951-8
US-11-176-951-9
US-11-176-951-9
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US-11-176-951-12
US-11-176-951-12
US-11-176-951-12
US-11-176-951-11
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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117, Appl
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116, Appl
117, Appl
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) Sequence 2, Application US/10522789
) Sequence 2, Application US/10522789
) Publication No. US20050260732A1
) GENERAL INFORMATION:
APPLICANT: TANABE SEIYARU CO., LTD.
TITLE OF INVENTION: Three-dimensional structure of dipeptidyl peptidase IV
FILE REFERENCE: 03-039-ECT
CURRENT APPLICATION NUMBER: US/10/522,789
CURRENT PILING DATE: 2002-01-28
) PRIOR PILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 2
) SOFTWARE: Patentin version 3.1
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US-11-077-550-155
US-11-077-550-165
US-11-077-550-62
US-11-077-550-62
US-11-077-550-63
US-11-077-550-64
US-11-077-550-68
US-11-077-550-68
US-11-077-550-68
US-11-077-550-16
US-11-077-550-16
US-11-077-550-16
US-11-077-550-14
US-11-077-550-14
US-11-077-550-14
US-11-077-550-18
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Best Local Similarity 100.
Matches 728; Conservative
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JUNEARL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

TITLE OF INVENTION: THERAPY OF COLON CANCER

TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERRICE: MPMO1-029PRNM

CURRENT FALLING DATE: 2005-07-21

PRIOR PELING DATE: 2001-12-10

PRIOR PELING DATE: 2002-03-05

PRIOR PELING DATE: 2002-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR PELING DATE: 2002-05-20

MINDER PELING DATE: 2002-05-20
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                 275 VTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN 334
                                                                                             CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKXDCTFIT 394
                                                                                                                                                         KGTWEVIGIEALISDYLYYISNEYKGMPGGRNLYKIQLSDYTKYTCLSCELNPERCQYYS 432
                                                                                                                                                                                VSPSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDPII 492
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                                                                          CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo Sapiens
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LENGTH: 760
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                                                                                                                                                                                                                                                                                                                               613 VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
KGTWEVIGIBALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
                         399 KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
                                                                              433 VSPSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKQLDFII
                                                                                                    459 VSFSKBAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFII
                                                                                                                                                                                                                                            DGRGSGYQGDKIMHAINRRLGTFBVBDQIEAARQFSKWGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                                                               LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic; ; OTHER INFORMATION: construct
US-11-116-939-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-11-116-939-13
is Gaquence 13, Application US/11116939
is Publication No. US20050265995A1
is GENERAL INFORMATION:
is APPLICANT: Stephen Tomlinson
is APPLICANT: Richard J. Quigg
ittle OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
if PILE REPREEMENT 19113-10115U-399
icurrent APPLICATION NUMBER: US/11/116,939
icurrent FILING DATE: 2005-04-28
is PRIOR FILING DATE: 2004-04-28
is NUMBER OF SEQ ID NOS: 27
is SOCTHARE: FastSEQ for Windows Version 4.0
is SEQ ID NO 13
icingTH: 762
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74 DPDGPHSDRIYYLAMSGENRENTLFYSEIPKTINRAAVLMLSW-------KPLLDLFQA 125
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CURRENT FILING DATE: 2002-66-13
PRIOR APPLICATION NUMBER: US 09/797,039
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/797,039
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-66-15
PRIOR PILING DATE: 2001-66-15
PRIOR PILING DATE: 2001-66-15
PRIOR PILING DATE: 2001-66-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-08-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 DVGVDPQAMWYTDEDHGIASSTAHQHIYTHMSHFIKQCFSLP 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGVDFQAMMYTDEDHGIASSTAHQHIYTHMSHFIKQCFSLP 102
                                                                                                                                                                                                                                                                                                      Query Match
13.7%; Score 550; DB 7; I
Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, Inc.
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NUMBER OF SEQ ID NOS: 45
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/11151601
Publication No. US20060003413A1
GENERAL INFORMATION:
                 SOFTWARE: Patentin Ver. 3.3
                                                                                                                             TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-951-7
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Best Local Similarity
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                                                    SEQ ID NO 7
LENGTH: 102
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| Sequence 7. Application US/11176951
| Subjication No. US20060024313A1
| GENERAL INFORMATION:
| APPLICANT: CHEN, XIN
| TITLE OF INVENTION: PROLYL DIPEPTIDASES
| FILE REPRESENCE: 10842.0019
| CURRENT APPLICATION NUMBER: US/11/176,951
| CURRENT FILING DATE: 2004-07-06
| PRIOR FILING DATE: 2004-07-06
| PRIOR FILING DATE: 2004-07-06
| PRIOR FILING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 22
                                                        7;
                                                                                                                                                                                                                                                                                              62 VFLENSTFDEFGHSIN--DYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITE 119
                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ERIPNNTOWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 EVPSAYSALWWSPNGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKACAVNPT 239
204 EMLPTKYALWWSPNGKFLAYAEFNDKDIPVIAYSYYGDE--QYPRINIPYPKAGAKNPV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVM 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DICDYDESSGRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHIC 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 SICDFREDMQTWDCPKTQEHIEESRTGWAGGFFVSRPVFSYDAISYXIFSDXDGYKHIH 378
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                                                        Gaps
                                                        14;
        al Similarity 52.5%; Pred. No. 1e-160; 389; Conservative 138; Mismatches 200; Indels
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Best Local Similarity
Matches 389; Conserv
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Publication No. US20060024313A1
GENERAL INFORMATION:
APPLICANT: CHEN, XIN
APPLICANT: CHEN, YUAN-SHOU
TITLE OF INVENTION: PROLYL DIPEPTIDASES
FILE OF INVENTION: PROLYL DIPEPTIDASES
FILE NEFERENCE: 08442.0019
CURRENT APPLICATION NUMBER: US/11/176,951
CURRENT PILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 60/586,095
PRIOR APPLICATION NUMBER: 60/585,952
                                                                                                                                                                                  292 ILRILYBENDESEVEIIH---VTSPMLETRRADSFRYFKTGTANPKVTFKWSEIMIDAEG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566 DFPISKYSNQKNPH---C----VSLYKLSSPEDDPTCKTKEFWATILDSAGPLPDYTPPE 618
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Sequence 5, Application US/11176951

Publication No. US20060024313A1

GENERAL INFORMATION:

APPLICANT: CHEN, XIN.

APPLICANT: CHEN, YUAN-SHOU

TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF

TITLE OF INVENTION: DIPEPTIDASES

FILE REFRERCE: 08842.0019

CURRENT APPLICATION NUMBER: US/11/176,951

CURRENT APPLICATION NUMBER: 60/586,095

PRIOR PRILING DATE: 2004-07-06

PRIOR FILING DATE: 2004-07-06

PRIOR FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 3.3
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Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 54; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          10.2%; Score 410.5; DB 7; 72.3%; Pred. No. 2.7e-25; iive 17; Mismatches 10;
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; Sequence 1, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enz;
; FILE REFERENCE: GC511-PC7;
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 657
PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 8
LENGTH: 102
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                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 73; Conser
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NUMBER OF SEQ ID NOS:
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Publication No. US20060024313A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHEN, XIN
APPLICANT: CHEN, XIN
APPLICANT: GENOME AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF
TITLE OF INVENTION: PROLYL DIPEPTIDASES
FILE REFERENCE: 08842.0019
CURRENT APPLICATION NUMBER: US/11/176,951
CURRENT FILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 60/586,095
PRIOR PILING DATE: 2004-07-06
PRIOR FILING DATE: 2004-07-06
                                                               75 SINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWV---- 129
                                                                                                                            130 ----TWSPVGHKLAYVWNND----IYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEE 180
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                                    Gaps
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1 6.8%; Score 272; DB 7; Length 657; Similarity 20.4%; Pred. No. 2e-13; Conservative 113; Mismatches 285; Indels 20
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US-11-176-951-9
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Sequence 12, Application US/11176951
GENERAL INFORMATION:
Hublication No. US20060024313A1
GENERAL INFORMATION:
APPLICANT: CHEN, XIN
TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV PAMILY OF
TITLE OF INVENTION: PROLYL, DIPEPTIDASES
TILE REPERRENE: 08842.0019
CURRENT APPLICATION NUMBER: US/11/176,951
CURRENT APPLICATION NUMBER: 60/586,095
PRIOR PILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: 60/585,952
PRIOR PILING DATE: 2004-07-06
PRIOR PILING DATE: 2004-07-06
PRIOR PILING DATE: 2004-07-06
SHOW APPLICATION NUMBER: 60/585,952
PRIOR PILING DATE: 2004-07-06
SHOW APPLICATION NUMBER: 2005-07-06
SHOW APPLICATION NUMBER: 2
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Publication No. US20060024313A1
GENERAL INFORMATION:
APPLICANT: CHEN, XIN
APPLICANT: CHEN, YUAN-SHOU
TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF
TITLE OF INVENTION: PROLYL DIPEPTIDASES
FILE REFERENCE: 08842.0019
CURRENT APPLICATION NUMBER: US/11/176,951
CURRENT PILING DATE: 2005-07-06
PRIOR APPLICATION NUMBER: 60/586,095
PRIOR APPLICATION NUMBER: 60/585,952
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2 PSERYLGL----HGLDNRAYEMTKVAHRVSALEEQQFLIIHPTADEKIHFQHTAELITQL
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2 FSERYLGL----HGLDNRAYEMTKVAHRVSALEEQQPLIIHPTADEKIHFQHTAELITQL
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4.2%; Score 167; DB 7;
Best Local Similarity 32.4%; Pred. No. 2.7e-06;
Matches 33; Conservative 24; Mismatches 39
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4.2%; Score 167; DB 7;
Best Local Similarity 32.4%; Pred. No. 2.7e-06;
Matches 33; Conservative 24; Mismatches 39;
SOFTWARE: Patentin Ver. 3.3 SEQ ID NO 9
                                                                                  LENGTH: 115
TYPE: PRT
CRGANISM: Homo sapiens
US-11-176-951-9
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-11-176-951-10
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; Sequence 10. Application US/11176951
; Publication No. US20060024313A1
; GENERAL INFORMATION:
    APPLICANT: CHEN, YONN-SHOU
    TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF
    TITLE OF INVENTION: PROLYL DIPEPTIDASES
; FILE REPRENCE: 08842.0019
; CURRENT APPLICATION NUMBER: US/11/176,951
; CURRENT PILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: 60/586,095
; PRIOR PILING DATE: 2004-07-06
; PRIOR PILING DATE: 2004-07-06
; PRIOR PILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 10
; LENGTH: 109
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GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: CHEN, XIN

APPLICANT: CHEN, XIN

TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF

TITLE OF INVENTION: PROLYL DIPEPTIDASES

TITLE OF INVENTION: PROLYL DIPEPTIDASES

FILE REFERENCE: 08442.0019

CURRENT APPLICATION NUMBER: 60/586,095

PRIOR PELING DATE: 2004-07-06

PRIOR APPLICATION NUMBER: 60/586,095

PRIOR FILING DATE: 2004-07-06

PRIOR PILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIN Ver. 3.3

LENGTH: 27
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                                                                                                                                                                                                    Query Match 3.6%; Score 145; DB 7; Length 27; Best Local Similarity 100.0%; Pred. No. 2e-05; Matches 27; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 6
LENGTH: 27
                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-11-176-951-13
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Sequence II. Application US/11176951

| Sequence II. Application US/11176951
| Publication No. US20060024313A1
| GENERAL INFORMATION:
| APPLICANT: CHEN, XIN
| APPLICANT: CHEN, XUN-SHOU
| TITLE OF INVENTION: PROLYL DIPEPTIDASES
| TITLE OF INVENTION: PROLYL DIPEPTIDASES
| FILE REFERENCE: 08042_0019
| CURRENT APPLICATION NUMBER: US/11/176,951
| CURRENT FILING DATE: 2005-07-06
| PRIOR APPLICATION NUMBER: 60/586,095
| PRIOR APPLICATION NUMBER: 60/586,952
| PRIOR PRILING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: PatentIN Ver. 3.3
| SEQ ID NO 11
| LENGTH: 99
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APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Select. Oskar
APPLICANT: ALBERTANER, Oskar
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
CURRENT APPLICATION NUMBER: US/10/454,437
CURRENT FILING DATE: 1999-06-13
PRIOR PLLING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR PLLING DATE: 1999-07-08
PRIOR PLLING DATE: 1999-07-08
PRIOR PLLING DATE: 1999-07-08
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3.6%; Score 145; DB 7; Length 109; 33.7%; Pred. No. 0.00013;
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US-10-454-437-118
; Sequence 118, Application US/10454437
; Fublication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Prome Version of the Pompejus of the Pricant of 
                                                              Best_Local Similarity 33.74
Matches 33; Conservative
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373 KGTWEVIGIEALISDYLYYIS--NEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCOY 430
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PRIOR APPLICATION NUMBER: DE 19932126.4

PRIOR PILING DATE: 1999-07-09

PRIOR PLING DATE: 1999-07-19

PRIOR PLING DATE: 1999-07-19

PRIOR PLING DATE: 1999-07-09

PRIOR PLING DATE: 1999-07-09

PRIOR PLING DATE: 1999-07-04

PRIOR PLING DATE: 1999-07-14

PRIOR PLING DATE: 1999-07-14
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3.1%; Score 124; DB 6; Length 668;
Best Local Similarity 19.5%; Pred. No. 0.065;
Matches 101; Conservative 68; Mismatches 180; Indels 170; Gaps
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; ORGANISM: Corynebacterium glutamicum
US-10-454-437-118
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Search completed: February 15, 2006, 13:29:41 Job time : 19 secs

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APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIRROBLAST ACTIVATION PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
COUNTRY: USA
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100.0%; Pred. No. 3.7e-306;
iive 0; Mismatches 0;
                                  US-09-870-133-2

US-10-160-501-5

US-10-960-501-5

US-10-473-757-2

US-10-476-264-106

US-10-476-264-110

US-10-476-264-142

US-10-476-264-142

US-10-476-264-146

US-10-476-264-146

US-10-476-264-114

US-10-361-130-120

US-10-361-130-120
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/20,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020034789Alman D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 10D 5330.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
FILING DATE:
CLASSIFICATION:
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Patent No. US20020034789A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 728; Conservative
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Sequence 6, Appli
Sequence 922, App
Sequence 41, Appli
Sequence 6, Appli
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Sequence 863, App
Sequence 69, Appl
Sequence 70, Appl
Sequence 72, Appl
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Sequence 4, Appli
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Sequence 38, Appl
Sequence 1390, Ap
Sequence 3, Appli
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Sequence 590, App
Sequence 18, Appl
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Sequence 55, Appl
                                                                                                                                    February 15, 2006, 13:25:59; Search time 168 Seconds (without alignments) 1840.439 Million cell updates/sec
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': /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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': /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                 5.1.7
Biocceleration Ltd.
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US-10-993-959-1

US-10-952-459-18

US-10-631-467-565

US-10-002-593-6

US-10-165-603-6

US-10-423-714-6

US-10-423-714-6

US-10-424-147

US-10-744-147

US-10-770-712-1

US-10-770-770-770-1

US-10-770-770-770-1

US-10-770-770-770-1
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                 GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match 1
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Sequence 590, Application US/10295027

Publication No. US20030232350A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Glabsery, Wendy M.

APPLICANT: Glynne, Richard

APPLICANT: Hevezi, Peter A.

APPLICANT: Hevezi, Peter A.

APPLICANT: Mark, David H.

APPLICANT: Watson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Bos Biotechnology, Inc.

APPLICANT: Bos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
                                                                                                                                                       VTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTBNIIVASF
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                                                    SKKTYTLTDYLKNTYRLKLYSLRMISDHBYLYKQENNILVPNAEYGNSSVFLENSTFDEF
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                                                                                                                                           PVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEEVFSAYSALWWSP
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                                     SRKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEF
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Pred. No. 3.7e-306;
Hismatches 0;
Local Similarity 100.0%; P
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                                                                                                                                                                                                                                                                                                KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
                                                                                                                                                                                                                                                                                                               KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
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                                                       GHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTWS
                                                                                                          159 PVGHKLAYVANNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEFVFSAYSALWWSP
                                                                                                                                                         VSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFII
SRKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNARYGNSSVFLENSTFDEF
                                        CHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTWS
                                                                                                                                            NGTPLAYAQPNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKPFVVNTDSLSS
                                                                                                                                                                                              VTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVMDICDYDESSGRWN
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Publication No. US20030165489A1
GENERAL INFORMATION:
APPLICANT: Grouzmann, Eric
APPLICANT: Lacroix, Jean-Silvain
APPLICANT: Mondow, Michal
TILLE OF INVENTION: Whethod of Treating Rhinitis and Sinusitis
FILE REFERENCE: 81985/276823
CURRENT APPLICANTION: WHERE: US/09/993,959
CURRENT FILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
SEQ ID NO 1
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ORGANISM: Homo sapiens
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Publication No. US20050074805A1
GENERAL INFORMATION:
APPLICANT: Kochan, Jarema Peter
APPLICANT: Rosinski, James Andrew
TITLE OF INVENTION: Specific Markers for Diabetes
FILE REFERENCE: 21270US1
CURRENT APPLICATION NUMBER: US/10/952,459
CURRENT APPLICATION NUMBER: US/10/952,459
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
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98.0%; Score 3939; DB 5; L
Best Local Similarity 100.0%; Pred. No. 3.7e-306;
Matches 728; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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98.0%; Score 3939; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.7e-306;
Matches 728; Conservative 0; Mismatches 0;
FILE REPERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/63,733
PRIOR PILING DATE: 2000-09-15
PRIOR PELING DATE: 2000-09-15
PRIOR PELING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-13
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PRIOR PELING DATE: 2001-10-08
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-3
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US-10-002-593-6

Sequence 6, Application US/10002593

Sequence 6, Application US/10002593

Sequence 6, Application O. US20020137120A1

Sequence 6, Application O. US20020137120A1

GENERAL INFORMATION:

APPLICANT: Vanderbilt University

APPLICANT: Brown, Nancy J.

TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA

TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA

TITLE OF INVENTION UNMER: US/10/002,593

CURRENT APPLICATION NUMBER: US/10/02,593

CURRENT PELICATION NUMBER: 60/244,524

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 10

SEQ ID NOS: 10

LENGTH: 766
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                                                                                                             LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
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                                                                                         LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
                                VSPSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLBDNSALDKMLQNVQMPSKKLDFII
                                                VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
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US-10-002-593-6
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759 IKQCFSLP 766
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; Publication No. US20050208496A1
; GENERAL INFORMATION:
    APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive prints OF INVENTION: disease
; TITLE OF INVENTION: Method for 10/0/631,467
; TITLE OF INVENTION: Method for 10/0/631,467
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: UP 2003-023-20
; PRIOR PILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SEQ ID NO 565
; ENGTH: 766
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Best Local Similarity 100.0%; Pred. No. 3.7e-306;
Matches 728; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
US-10-631-467-565
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Sequence 6, Application US/10423714

Sequence 6, Application US/10423714

Publication No. US20030180828A1

GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Brown, Mancy J.
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ANGIOTENSIN CONVERT:
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ANGIOEDEMA
FILE REFRENCE: Atv Docket No. US20030180828A1 1242/48/2
CURRENT APPLICATION NUMBER: US/10/423,714
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: 60/244,524
PRIOR APPLICATION NUMBER: 60/244,524

NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1

SEQ ID NO 6
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     NGTFLAYAQFNDTEVPL1EYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
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759 IKQCFSLP 766
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ORGANISM: Homo sapiens
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US-10-423-714-6
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                                                                                       KGTWEVIGIBALTSDYLYYISNEYKGMPGGRNLYKIQLIDYTKVTCLSCELNPERCQYYS
                                                                                                                                                                                                   LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVPRLNWATYLASTENIIVASF
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                                                                  KGTWEVIGIBALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
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| Publication No. US20030021792A1
| GENERAL INFORMATION: | FUBLICANT: Rober, Paul W. |
| APPLICANT: Rebens, Paul W. |
| APPLICANT: Stevens, Anthony C. |
| TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE |
| TITLE OF INVENTION: PROTEINS |
| TITLE OF INVENTION: PROTEINS |
| TITLE OF INVENTION: PROTEINS |
| FILE REFERENCE: TPTECH.001A |
| CURRENT FILING DATE: 2001-06-07 |
| PRIOR APPLICATION NUMBER: 60/297,021 |
| PRIOR PILING DATE: 2001-06-08 |
| PRIOR FILING DATE: 2001-07-12 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: PastSEQ for Windows Version 4.0 |
| LEATH: 766 |
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Best Local Similarity 99.9
Matches 727; Conservative
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US-10-165-603-7
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GHSINDYSISPDGQFILLEYNYVKQWRHSYTASYDIYDLNKRQLITEERIPNNTQWVTWS 158
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APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kutz C.
APPLICANT: Gish, Kutz C.
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APPLICANT: Gish, Kutz C.
APPLICANT: Gish, Kutz C.
APPLICANT: Gish, Kutz C.
APPLICANT: Herer A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Machon, Susan R.
APPLICANT: Machon, Sor Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 60/663,733
PRIOR PILING DATE: 2000-09-15
PRIOR PLING DATE: 2000-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-15
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                                                                                                                                                                      CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEBGYRHICYFQIDKKDCTFIT
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                                                                                    NGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
                                                                                                                       VTINATSIQITAPPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN
                                                                                                                                     VINATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVWDICDYDESSGRWN
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                                                                                                                                                                                                                       KGTWEVI GI BALTSDYLYYI SNEYKGMPGGRNLYKI QLSDYTKVTCLSCELNPERCQYYS
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                        PVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEEEVFSAYSALWWSP
                                                                       NGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
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132 192 218 312 372 398 492 518 552 578 612 672 732 158 252 278 KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS 432 458 72 98 CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT EXILIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF VTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWN CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT VSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFII LNETKFWYQMILPPHFDKSKKYPLILDVYAGPCSQKADTVFRLNWATYLASTENIIVASF VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV PVGHKLAYVMNNDIYVKIEDNIPSYRITWTGKEDIIYNGITDWYYEEEVFSAYSALWWSP NGTFLAYAQFNDTEVPLIEYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFPVVNTDSLSS SKKTYTLTDYLKUTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEF DGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM SRKTYTLTDYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEF Gapa PALM. PRIOR APPLICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-29

PRIOR FILING DATE: 2001-11-29

PRIOR PLICATION NUMBER: US 60/340,376

PRIOR PLICATION NUMBER: US 60/347,211

PRIOR PLICATION NUMBER: US 60/347,211

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-10

PRIOR FILING DATE: 2002-01-10

PRIOR FILING DATE: 2002-0-1-10

PRIOR PLICATION NUMBER: US 60/355,250

PRIOR PLICATION NUMBER: US 60/356,714

PRIOR FILING DATE: 2002-02-13

PRIOR FILING DATE: 2002-02-13

REMAINING DATE: 2002-02-13

REMAINING PAPELCATION NUMBER: US 60/356,714

PRIOR FILING DATE: 2002-02-13

SECTION NUMBER OF SEQ ID NOS: 1386

SOFTWARE: PALENTIN VET: 2.1

FERMALLIAND FOR SEQ ID NOS: 1366

SOFTWARE: PALENTIN VET: 2.1 ° Length 766; Indels 97.8%; Score 3933; DB 4; 99.9%; Pred. No. 1.1e-305; ive 0; Mismatches 1; Query Match 97.8 Best Local Similarity 99.9 Matches 727; Conservative ; ORGANISM: Homo sapiens US-10-295-027-922

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RESULT 11

US-11-041-674-6

US-11-041-674-6

Sequence 6, Application US/11041674

Publication No. US2050181468A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/11/041,674

CURRENT APPLICATION NUMBER: US/11/041,674

CURRENT FILING DATE: 2000-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR FILING DATE: 2001-10-31

PRIOR PRILING DATE: 2003-4-25

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1

LENGTH: 766
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                   699 EYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMMYTDEDHGIASSTAHQHIYTHMSHF
    673 EYLLIHGTADDNVHPQQSAQISKALVDVGVDFQAMMYTDEDHGIASSTAHQHIYTHMSHP
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                                                                                                                                    Sequence 41, Application US/10794899; Publication No. US20040146516A1; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Lumen-Exposed Molecules and FILE REFERENCE: 27110-715; CURRENT FILING DATE: 2004-03-05; NUMBER OF SEQ ID NOS: 121; SOFTWARE: Patentin version 3.1
SEQ ID NO 41; LUMGTH: 766
                                 740
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US-10-794-899-41
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US-10-794-899-41
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               CLVARQHIEMSTIGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT
                                                                                                    KGTWEVIGIEALTSDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
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US-10-770-712-1
; Sequence 1, Application US/10770712
; Publication No. US20050170333A1
; GENERAL INFORMATION:
; APPLICANT: VOIGAIL, Aristo
; TILLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCIZ.008A
; CURRENT PILING DATE: 2004-02-03
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 766
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Pred. No. 2.3e-305;
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Best Local Similarity 99.7%;
Matches 726; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-770-712-1
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519 LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF 578
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                                                                         DGRGSGYQGDKIMHAINRRLGTFBVBDQIBAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                                                      639 VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
                                                                                                                                                                                                               EXLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF
                                                                                                                                                                                                                                      39 SRKTYTLTDYLKOTYRLKLYSLRMISDHEYLYKQENNILVFNAEYGNSSVFLENSTFDEF
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                                                                                                                             613 VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
                                           DGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
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Publication No. US20050123910A1

GENERAL INPORMATION:
APPLICANT: Cooken, William Osmond Charles Michael
APPLICANT: Allen, Maxine
APPLICANT: Allen, Maxine
APPLICANT: Allen, Maxine
APPLICANT: Allen, Maxine
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: US/10/476,264
CURRENT PILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB0110044.5
PRIOR APPLICATION NUMBER: GB011004.5
PRIOR APPLICATION NUMBER: GB011004.5
PRIOR APPLICATION NUMBER: GB0124594.3
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-10-12
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97.7%; Score 3929; DB 5;
Best Local Similarity 99.7%; Pred. No. 2.3e-305;
Matches 726; Conservative 1; Mismatches 1;
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US-10-476-264-147
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US-10-476-264-147
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                                                                                                                                               457 YYSVSLSKEAKYYQLGCRGPGLPLYTLHRSTDQKELRVLEDNSALDKMLQDVQMPSKKLD
                                                                                                                                                                                                                                                           277 TITIPMQITAPASVITGDHYLCDVAWVSEDRISLQMLRRIQNYSVMAICDYDKTTLVWN
                                                                                       ASFDGRGSGYQGDKIMHAINKRLGTLEVEDQIEAARQFLKMGFVDSKRVAIWGWSYGGYV
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APPLICANT: Roben, Anthony C.
TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: TPTECH.001A
CURRENT APPLICATION NUMBER: US/10/165,603
CURRENT APPLICATION NUMBER: 60/297,021
PRIOR APPLICATION NUMBER: 60/297,021
PRIOR APPLICATION NUMBER: 60/305,117
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PREUSE (FOR WINDOWN VERSION 4.0)
SEQ ID NO SEQ ID NOS: 31
LENGTH: 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-165-603-4
; Sequence 4, Application US/10165603
; Publication No. US20030021792A1
; GENERAL INFORMATION:
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                                                            CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKOCTFIT
                                                                                                                  399 KGTWEVIGIEALTSDYLYYISNEYKGWPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
                                                                                                                                                        VSFSKRAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLRDNSALDKMLQNVQMPSKKLDFII
                                                                                                                                                                       LINETKEWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADIVFRLNWATYLASTENIIVASF
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84.7%; Pred. No. 1.6e-263;
ive 52; Mismatches 57; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2. Application US/10770712
Publication No. US2005017033A1
GENERAL INFORMATION:
APPLICANT: Voidami, Aristo
TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
FILE REFREENCE: IMSCII. 008A
CURRENT APPLICATION NUMBER: US/10/770,712
CURRENT FILING DATE: 2004-02-03
NUMBER OF SEQ ID NOS: 133
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Rattus norvegicus US-10-770-712-2
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Best Local Similarity 84.7%
Matches 618; Conservative
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IKQCFSLP 766
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US-10-770-712-2
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                                              253 VTNATSIQITAPASMLIGDHYLCDVTWATQERISLOWLRRIQNYSVMDICDYDESSGRWN 312
                                                                      CLVARQHIEMSTIGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKD---CT 369
                                                                                                                   430 YYSVSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLD 489
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Search completed: February 15, 2006, 13:29:19 Job time : 171 secs

Sequence 45296, A Sequence 19472, A Sequence 1, Appli Sequence 1, Appli Sequence 33, Appl Sequence 30, Appl Sequence 19924, A

Sequence 29, Sequence 28, Sequence 11, Sequence 4529

Sequence Sequence Sequence

Sequence

30, Appl 19924, A 3, Appli 23, Appl

Sequence

Sequence

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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98.0%; Score 3939; DB 4; Length 755; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
COUNTRY: Boston
COUNTRY: Boston
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
                           US-10-401-436-3

US-09-518-550-42

US-09-518-550-29

US-09-518-550-29

US-09-079-522-11

US-09-248-796-4-12

US-09-976-674-1

US-09-976-674-1

US-09-976-674-35

US-09-976-674-35

US-09-518-550-30

US-09-248-796A-19924
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US-09-976-674-27
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frager, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 00530/055002
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-PEB-1992
ATTORNEY/AGENT INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 728; Conservative
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PCT-US93-07923-3
STRANDEDNESS
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PCT-US93-07923-3
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Sequence 2, Appli
Sequence 2, Appli
Sequence 26, Appl
Sequence 8330, Ap
Sequence 5, Appli
Sequence 4, Appli
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Sequence 6, Appli
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Sequence 7, Appli
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                                                                                                   February 15, 2006, 13:14:53 ; Search time 48 Seconds (without alignments) 1274.583 Million cell updates/sec
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Sequence 4, A
Sequence 41,
Sequence 43,
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(Ggn2_6/ptodata/1/iaa/5_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/H_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/RE_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/RE_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/RE_COMB.pep:*
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PCT-US93-07923-2

US-08-230-491A-3

US-08-619-280A-3

US-08-940-316-1

US-09-794-236-1

US-09-949-016-10450

US-09-949-016-10460

US-09-949-016-10460

US-09-949-016-10460

US-09-95-18-550-27

PCT-US93-07923-11

US-08-619-280A-2

US-08-619-280A-2

US-08-619-280A-2

US-08-910-016-8330

US-09-949-016-8330

US-09-949-016-8330

US-09-976-674-41

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             GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 CLVARQHIEMSTIGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 NGTFLAYAQFNDTEVPLIBYSFYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 KGTWEVIGIEALISDYLYYISNEYKGMPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYS
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 05-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: FRASET, 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 34,819
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         00530/055002
                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
PCT-US93-07923-2
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                                                                       GHSINDYSISPDGQFILLERYNYVKQMRHSYTASYDIYDLNKRQLITEBRIPNNTQWVTWS
                                                                                                                                                                       148 PVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYBEBVFSAYSALWWSP
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                     SRKTYTLTDYLKNTYRLKLYSLRWISDHBYLYKQENNILVFNABYGNSSVFLENSTFDBF
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Sequence 2, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUVTRY: U.S.A.
ZIP: O2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BS52 Model 502 or 555X
OPPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
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APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
ITILE OF INVENTION: ALPHA, AND USES THEREOF
ITILE OF INVENTION: ALPHA, AND USES THEREOF
INTHER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STARET: 805 Third Avenue
CITY: New York City
STARET: 805 Third Avenue
CITY: New York City
STARET: BOS Third Avenue
CITY: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: 08/08/619,280A
FILING DATE: 18-MACH-1996
CLASSIFICATION NUMBER: US/08/619,280A
FILING DATE: 20-APPLICATION
FILING DATE: 20-APPLICATION
FILING DATE: 20-APPLICATION
FILING DATE: 20-APPLICATION
FILING DATE: 10-APPLICATION
                                                                                                   CLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKKDCTFIT
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1UD 5330.1
TELECHONE: (212) 688-9200
TELEPPA: (212) 688-9200
TELEPPA: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08619280A; Patent No. 5767242; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   733 IKOCPSLP 740
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                                                  692 BYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF
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                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08230491A
Patent No. 5587299
GENERAL INPORMATION
APPLICANT: Rettid, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.
TITLE OF INVENTION: FISHOBLAST ACTIVATION PROTEIN 'AND USES TITLE OF INVENTION: FISHOBLAST ACTIVATION PROTEIN 'AND USES TITLE OF INVENTION: THEREOF NUMBERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: FELFE & LYNCH
STREET: 805 THIRD AVENUE
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MABDIUM TYPE: DISKETTE 3.5 inch 1.2 MB
COMPUTER: IBM PS/2
SOBTWARE: IBM PS/2
SOFTWARE: WORDPERRECT - ASC II
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAWE: HAIBON, NO. 5587299man D.
REGISTRATION NUMBER: LUD 330
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEPAX: (212) 838-3884
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 766 amino acids
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Best Local Similarity 100.
Matches 728; Conservative
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752 IKQCFSLP 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
COUNTRY:
                                                                                                                                                                                                                                                                                          US-08-230-491A-3
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                   VSFSKEAKYYQLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFII 492
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APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION
TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF
CORRESPONDENCE: 10
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                                                            Query Match
98.0%; Score 3939; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches
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Patent No. 5965373
GENERAL INFORMATION:
: 766 amino acids
amino acid
3Y: linear
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                       TOPOLOGY:
                               US-08-940-391-3
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279 VINATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVWDICDYDESSGRWN
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100.0%; Pred. No. 0;
ative 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,391
FILING DATE: 01-0CT-1997
CLASSIFTCATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/619,280
FILING DATE: 18-WARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRL-1994
ATTORNE: HANSON, NO. 5965373man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 10,944
ATTORNE: HANSON, NO. 5965373man D.
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                 ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
Third Avenue ork City
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 728; Conservative
                CITY: 805 Thir CITY: New York C. STATE: New York COUNTRY: USA
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                         519 LNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
                                                                                             DGRGSGYQGDKIMHAINRRLGTPEVEDQIEAARQPSKMGFVDNKRIAIWGWSYGGYVTSM
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     LINETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWATYLASTENIIVASF
                                                                       DGRGSGYQGDKIMHAINRRLGTPEVEDQIEAARQFSKMGFVDNKRIAIWGWSYGGYVTSM
                                                                                                                                         VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENPKQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Rettig; Volfgang, Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSEE: Palfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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100.0%; Pred. No. v.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, NO. 6846910man D. REGISTRATION NUMBER: 30,946 REPERNICE/DOCKET NUBBER: LUD 5330.1 TELECOMMUNICATION: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,286
FILING DATE: 18-WARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09265606 Patent No. 6846910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3884
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acids
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759 IKQCFSLP 766
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Best Local Simil
Matches 728; (
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Patent No. 6337069

GENERAL INFORMATION:

APPLICANT: Grouzmann, Bric

APPLICANT: Lacroix, Jean-Silvain

APPLICANT: Monod, Mitchel

TITLE OF INVENTION: Method of Treating Rhinitis and Sinusitis

FILE REFERENCE 81985/276823

CURRENT APPLICATION NUMBER: US/09/794,236

CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.0
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Matches 728; Conservative 0; Mismatches
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Sequence 6, Application US/10002593

Patent No. 6586198
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Brown, Nancy J.
APPLICANT: Brown, Nancy J.
TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIR-
TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIR-
TITLE OF INVENTION: BIOLOGICAL MARKERS AND USOPERFIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
FILE REFERENCE: Atty Docket US/10/002,593
CURRENT FAPLICATION NUMBER: US/10/002,593
FRIOR APPLICATION NUMBER: 60/244,524
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US-09-949-016-10450
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Best Local Simil
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Sequence 10450, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, D. Craig et al.

APPLICANT: VENTER, D. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-07

PRIOR REPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FaetSEQ for Windows Version 4.0

SEQ ID NO 10450

LENGTH: 775

TYPE: PRI
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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ive 0; Mismatches
                   FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 6146
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.9'
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Patent No. 6812339
GENERAL INFORMATION: 681231
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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Pred. No. 0;
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 766
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ORGANISM: Homo sapiens
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APPLICANT: POTEMPA, Jan
APPLICANT: PANDILA, Jan
APPLICANT: PANDILA, Jan
APPLICANT: BANBULA, Jan
TITLE OF INTERNICE: 235.00190101
CURRENT APPLICATION NUMBER: 05/09/518,550
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/123,148
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 48
SOFTHARE: PALENTIN Ver. 2.1
SEQ ID NO 27
LENGTH: 766
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Pred. No. 0;
                                                                                                                                                  Sequence 27, Application US/09518550 Patent No. 6875851 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  726; Conservative
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US-09-518-550-27
                                              740
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                                                733 IKQCFSLP
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                                                                                                                                       US-09-518-550-27
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Best Local S
Matches 726
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                                                 Sequence 6.897679

Batent No. 6897679

GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Brown, Nancy J.
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
TITLE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA
TITLE OF INVENTION: 1001001/423,714
CURRENT APPLICATION NUMBER: 60/244,524
PRIOR APPLICATION NUMBER: 60/244,524
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 6.
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Matches 727; Conservative
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                   US-10-423-714-6
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279 VINATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVWDICDYDESSGRWN 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08230491A

Patent No. 5587299
GENERAL INFORMATION:
APPLICANT: Retig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Retig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Retig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Gaxin-Cheea, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: LBM PS/2

COMPUTER: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: DISKETTE 3.5 inch 1.2 MB STORAGE
COMPUTER: DISKETTE 3.5 inch 1.2 MB STORAGE
SOFTWARE: WORDPERRECT - ASC II
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,491A
FILING DATE: 20-APRIL-1994
CLASSIPICATION: 435
ATCHASIPICATION: WORDER: JUD 330
REGISTRATION NUMBER: JUD 330
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
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EYLLIHGTADDNVHFQQSAQISKALVDVGVDFQAMMYTDEDHGIASSTAHQHIYTHMSHF
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                                                                                             639 VLGSGSGVFKCGIAVAPVSRWEYYESVYTERYMGLPTBEDNLDHYRNSTVMSRAENFKQV
                                                                                                                                                      EYLLIHGTADDNVHPQOSAQISKALVDVGVDFQAMWYTDEDHGIASSTAHQHIYTHMSHF
                                                                    VLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYRNSTVMSRAENFKQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS FOR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZUBERT STANDARDE FORM:
MEDION TYPE: 3.5" DISkette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00530/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application PC/TUS9307923
GENERAL INFORMATION:
APPLICANT: Morimoto, Chikao
APPLICANT: Schlossman, Stuart F.
APPLICANT: Tanaka, Toshiaki
TITLE OF INVENTION: HUMAN CD26 AND MET
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,162
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: 07/832,211
FILING DATE: 06-PEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janie K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 555; Conservative
                                                                                                                                                                                                                                             733 IKOCFSLP 740
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PCT-US93-07923-11
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                                                                                                                                                                        120 BRIPNNTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIIYNGITDWVYEE 179
                                                                                                                                                                                                                                                                          VKFFVVNTDSLSSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVM 299
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                                                                                                                                                                                                                                                                                                                                       319 SICDFREDWQTWDCPKTQEHIEESRTGWAGGFFVSRPVFSYDAISYXKIFSDKDGYKHIH 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                          QNVQMPSKKLDFIILNETKFWYQMILPPHFDKSKKYPLLLDVYAGPCSQKADTVFRLNWA 538
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Patent No. 5767242
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Zimmermann, Rainer; Park, John E.;
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                 14;
                        Length 760;
                                              Indels
                                                Conservative 138; Mismatches 200;
                       53.9%; Score 2168; DB 1; 52.5%; Pred. No. 9.9e-182;
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738 GLSTNHLYTHMTHFLKOCFSL 758
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STREET: 805 Third Avenue
CITY: New York City
                                   Best Local Similarity
Matches 389; Conserv
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62 VFLENSTFDEFGHSIN--DYSISPDGQFILLEYNYVKOWRHSYTASYDIYDLNKRQLITE 119
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Best Local Similarity 52.5%; Pred. No. 9.9e-182;
Matches 389; Conservative 138; Mismatches 200;
                                     뜻
                                 Diskette, 3.5 inch, 2.0
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280A
FILING DATE: 18-WARCH-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30,946
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (212) 688-9200
TELEPRAS: (212) 688-9200
TELEPRAS: (212) 688-9200
TELEPRAS: (212) 838-384
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARRACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
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US-08-619-280A-2
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        QY
        599 AIWGWSYGGYVTSWVLGSGSGVFKCGIAVAPVSRWEYYDSVYTERYMGLPTPEDNLDHYR 658

        Db
        619 AIWGWSYGGYVSSIALASGTGLFKCGIAVAPVSSWEYYASVYTERPWGLPTKDDNLEHYK 678

        QY
        659 NSTVWSRAENFKQVEXLIHGTADDNVHFQQSAQISKALVDVGVDFQAMWYTDEDHGIAS 718

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        Db
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        QY
        719 STAHQHIYTHMSHPTKQCFSL 739

        Db
        738 GLSTNHLYTHWTHPLKQCFSL 758
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Search completed: February 15, 2006, 13:16:21 Job time : 51 Becs

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BX399854 BX399854
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AL548644 AL548644
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AU122649 AU122649
BQ937942 ACBROCOURT
AL533051 AL553051
AU139683 AU139683
CB957930 ACBROCOURT
BX496051 DKFZp779P
BX397280 BX397280
AV402291 Homo sapi
AY402292 Pan trogla
AX502292 Pan trogla
AL550603 AL550603
                                                                  February 17, 2006, 04:32:36; Search time 8805 Seconds (without alignments) 11605.109 Million cell updates/sec
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Match Length DB
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9b_est2::*

9b_htc::*:

9b_est4::*

9b_est5::*

9b_est7::*

9b_gss1::*

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Perfect score:
Sequence:
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CR860150 Pongo pygmaeus mRNA; cDNA DKFZp469P1419 (from clone DKFZp469P1419). CR860150. CR860150.1 GI:55731156 HTG. Pongo pygmaeus (orangutan) Pongo pygmaeus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;	Hominidae; Pongo. 1 (bases 1 to 3411) Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.	The German cDNA Consortium Direct Submission Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg. GREMANY	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ); Email s.wiemann@dkz-heidelberg.de; Seguenced by DKFZ (German Cancer Research Center.) Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKF2p469P1419) is available at the KZPD Deutsches Reseourcententum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469P1419 Further information about the clone and the sequencing project is available at http://ming cgf de/products/cdna/cdna/	Location() (mips 591.10) projects) comes. 1. 3411	/noce="u.peptinyi peptinase iv (nomo sapiens)" 13hPxpp469P1419" 632360 /gene="DKPZp469P1419"
RESULT 1 CR860150 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE	CONSRIM TITLE JOURNAL	COMMENT	FEATURES BOUTGE	gene

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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Langawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
    transcriptome based on functional annotation
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Nature 420, 563-573 (2002)
6 (bases 1 to 3289)
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GTCCTGGGATCGGGAAGCGGCGTGTTCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCGG 2033
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Mus musculus 0 day neonate kidney CDNA, RIKEN full-length enriched
library, clone:D630017G05 product:dipeptidylpeptidase 4, full
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Functional annotation of a full-length mouse cDNA collection
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/mol_type="genomic DNA"
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                                                                                                               1748 ACCAAGGAGATAAGATCATGCAATCAACAGAAGACTGGGAACATTTGAAGTTGAAG 1807
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Pan troglodytes
Eukaryotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Pan.
I (basea I to 2193)
Clark, A.G. (alanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Fodd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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Science 11.05
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2 (bases 1 to 2193)
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Reritera,B., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Direct Submission
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These sequences were made by sequencing genomic exons and or them based on alignment.

Location/Qualifiers
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AY418370 2191 bp DNA linear GSS 17-DEC-2003
Mus musculus DPP4 gene, VIRTUAL TRANSCRIPT, partial sequence,
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These sequences were made by sequencing genomic exons and ordering them based on allgnment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Ahng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia;
Schurognathi; Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 AGTGTCACCTGACCGACTGTTTGTTCTCTTGGAATACAACTACGTGAAGCAATGGAGAA
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/gene="DPP4"
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                                  GCTATTTCCAAATAGATAAAAAGACTGCACATTTATTACAAAAGGCACCTGGGAAGTCA
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                                                                                                                                                                                                                                                             864 TATTTGTGACTATGATGAATCCAGTGGAAGATGGAACTGCTTAGTGGCACGCAACACAT 923
                                                                                                                    984 TGATGGTAATAGCTTCTACAAGATCATCAGCAATGAAGAAGGTTACAGACACATTTGCTA
                   AGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTCTCCAAACGGCACTTTTTTAGCATATGC
                                                                       CCAGTTTAACGACACACAGGAGTGCCGCTCATTGAATACTCCTTCTATTCTGATGAGTCACT
                                                                                                                                         684 AAAGTTCTTTGTTAAATACAGACTCTCTCAGCTCAGTCACCAATGCAACTTCCATACA
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                                     AGTCTTCGGTGCCTACTCTGCACTGTGGTGGTCTCCAAACAACAACGTTTCTAGCTTATGC
                                                                                                                                                                               AATCACTGCTCCTGCTTCTATGTTGATAGGGGATCACTTGTGTGATGTGACATGGGG
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2049 2003 2063 2110 GGCAGATGATAATGTTCACTTTCAGCAGTCACTCAAAGCCCTGGTGGATGC 2169 1630 ATATGCAGGTCCCTGTAGTCAAAAGCAGATGCTTCCTTCAGACTGAACTGGGCCACTTA 1689 EST 30-MAR-2004 ALSS4569 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CON ALSS4569 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA ALSS4569 cacadadecerracardecercecaarrecadaadaacaacerreacearracadaaacre 2050 AACAGTCATGAGCAGAGCTGAACATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAAC AGGAGATAAGATCATGCATGCAATCAACAGAAGACTGGGAACATTTGAAGTTGAAGATCA CCTTGCAAGCACAAAAACATTATAGTAGCTAGCTTTGATGGCAGAGGAAGTGGTTACCA AATTGAAGCAGCCAGACAATTTTCAAAATGGGATTTGTGGACAACAAAGGAATTGCAAT TTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGGTCCTGGGATCGGGAAGTGGCGT TIGGGGCTGGTCATATGGAGGGTATGTAACCTCCAATGGTCCTGGGATCGGGAAGTGGCGT GITCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCGGTGGGAGTACTATGACTCAGTGTA GTTCAAGTGCGGAATAGCTGTGGCACCTGTGTCACGGTGGGGAGTACTATGACTCAGTGTA CACAGAACGTTACATGGGTCTCCCAAACTCCAGAAGACAACCTTGACCATTACAGAAATTC AACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAAC AGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCAGATCTCCCAAAGCCCTGGTCGATGT For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI083CC04QP1&c=1082.r. Location/Qualifiers

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                       EST 01-MAY-2004
                                                                                                                                                                                                                                                                                                  BX399854 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI0847J15 3-PRIME, mRNA sequence.
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/db_xxef=taxon:96084V15"
/clone="CSODIOB4V15"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                 CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATYCGCAATGAA
                            CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA
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Li Massa 1 to 987)

Li W Bs. Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

On May 13, 2003 his sequence version replaced gi:30629915.

Contact: Genoscope
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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; Pred. No. 3e-264;
10; Mismatches 3; Indels
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Matches 1048; Conservative
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF032ZD12_AF03069_2&c=1082.r
                                                                                                                                                                                                                                                                                      /clone="CSODIO84VJ15"
/clone Type="PLACENTA COT 25-NORMALIZED"
/clone Lib="Home sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enrichced, double-errand cDNA was
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                          GTGGTTACCAAGGAGATAAGATCATGCATGCAATCAACAGAAGACTGGGAACATTTGAAG
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Li,W.B., Gruber,C., Jessee,J. and Polayes,
Full-length cDNA libraries and normalizati
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
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AL541949 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE007YN21
F-PRIME, mRNA sequence.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                      231 TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTCGAGAACAGTACATTTGATGAGTTT
                                                                                          GGACATTCTATCCATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC
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                                                                                                                                          241 AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAAT
                                                                                                                                                                AAAAGGCAGCTGATTACAGAAGAGAGGTTCCAAACAACAACACAGTGGGTCACATGGTCA
                                                                                                                                                                                                                                       471 CCAGTGGGTCATAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCA
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1 (bases 1 to 1022)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
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I (bases 1 to 1014)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31270470.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: sequencagenoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a Notl-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                   AL548644
AL548644 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI036YE04 5-PRIME, mRNA sequence.
                                                                                                                                       GATCTCCAAAGCCCTGGTCGATGTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGA 2099
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
CAACCTTGACCATTACAGAAATTCAACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGT
                                                                    TGAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCA
                  720 TGAGTACCTNCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCA
                                                                                                                                                                780 GATCTCCAAGCCCTGGTCGATGTTGGAAGTGGATTTCCAGGCAATGTGGTATACTGATGA
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95.7%; Pred. No. 4.2e-205;
ive 19; Mismatches 14;
                                                                                                                                                                                                                                              840 AGACCATGG-ATAGCTAGCAGCACACCACCAAC 873
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI036YE04"
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AL548644.3 GI:45749064
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Best Local Similarity 95.7%
Matches 871; Conservative
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Genoscope - Centre National de Sequencage

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Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Prive prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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ACENTA COT 25-NORMALIZED Homo sapiens CDNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not!-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                          TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG
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TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG
                                                                                         GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCAGCTCA
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1 (bases 1 to 1007)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31266300.
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Pred. No. 3.2e-199;
9; Mismatches 26; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                         841 AITCAGAACTAITCGGTCATGGATAITIGTGACTAIGAIGCAAAACTACCAGTGGAA
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/db_xref="taxon:9606"
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95.4%;
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Best Local Similarity 95.4
Matches 852; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODE007YN21"
/tissue Lype="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECRNY sites of the pCMVSPORT 6 vector.
Library was not normalized."
                     On Feb 15, 2001 this sequence version replaced gi:30546617.

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Genoscope - Centre National de Sequencage
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoNY sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                            This sequence belongs to sequence cluster 1082.r
For more information about this cluster, see
http://www.genoscope.cms.fr/cdna?s=CSODE007GG11QP1&c=1082.r.
_Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.8%; Score 803.2; DB 1
llarity 94.5%; Pred. No. 3.5e-201
Conservative 11; Mismatches 33
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Best Local Simil
Matches 843; C
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HII human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5' - & 3' end one pass sequencing: Helix
Research Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                    35.2%; Score 768.4; DB 1; 98.4%; Pred. No. 5.6e-192; ive 0; Mismatches 11;
                                                                                                                                                                                                                                    /organism="Homo sapiens"
|mol_type="makNA"
|db_xref="taxon:9606"
|clone="NAMMA1002805"
|tissue type="mammary gland"
|clone lib="mammary gland"
|note="Vector: pMB185FL3"
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Matches 797; Conservative
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       Іводаі, Т.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 846)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT
                                                                           234 TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT
                                                                                                                                              294 GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC
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AU122649.1 GI:10947365
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 897)

2 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

3 Li,W.B., Gruber,C., Jessee,J. and normalization

1 (published (2001)

On Feb 15, 2001 this sequence version replaced gi:31274865.

Contact: Genoscope

Contre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime and enrithed, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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ALSS3051.3 GI:45857821
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                                              CCATGTAGTCAAAAAGCAGACACTGTCTTCAGACTGAACTGGGCCACTTACCTTGCAAGC
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                                                 720
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12 (bases 1 to 900)

13 (bases 1 to 900)

14 (bases 1 to 900)

15 Inth-MGC http://mgc.nci.nih.gov/.

16 Intitutes of Health, Mammalian Gene Collection (MGC)

17 Contact: Robert Strausberg, Ph.D.

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@mail.nih.gov

18 Email: cgapbs-r@minih.gov

18 Email: cgapbs-r@minih.gov

18 Consortium (LLNL)

18 Consortium (LLNL)

18 Consortium (LLNL)

19 Cond through the I.M.A.G.E. Consortium/LLNL at:

18 High quality sequence stop: 639.

18 Localnih.Qualifiers
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/mol type="mRNA"
/db_xref="taxons"
/db_xref="taxons"
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/clone_lib="NHH MGC_7"
/note="Grgan: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
       CTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCCGGTGG
                                     CTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGAATACCCGTGGCGCCTGTATCCCGGTGG
                                                                                                                                     GAAGTCTATGACTCAATGT-CACAGAACGTTACATGGGTCTTCCAACTTCAGAAGACAAC
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CAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAACAG
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Contact: Takeo 1809ai
Connics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Pax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 712.6; DB 1;
Pred. No. 3.4e-177;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="PLACE1011107"
/tisme type="placenta"
/clone lib="PLACE1"
/note="Vector: pME18SFL3"
 AU139683.1 GI:11001204
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ilarity 99.4%;
Conservative 0
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                                      Homo sapiens
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                    AACGGCACTTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTASTTGAATA
                                                                                                                                                                       AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC
                                                                                                                                                                                                                       TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT
                                                                                                                                                                                                                                                                                                                         GGACATICTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC
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                                                                                                                         Length 897;
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                                                                                                                      Score 721; DB 1; L
Pred. No. 2.1e-179;
7; Mismatches 2;
 db_xref="taxon:9606"
                                                                                                                       Query Match
Best Local Similarity 98.3%;
Matches 762; Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Vesearch Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                 Hominidae; Homo.
1 (bases 1 to 791)
Ota T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAAGCAGCCAGACAATTTTCAAAAATGGGATTTGTGGACAACAACAAATTGCAATTT
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Search completed: February 17, 2006, 07:21:17 Job time : 8810 secs

Sequence 474460, Sequence 62484, A Sequence 6344, Ap Sequence 6364, Ap Sequence 6364, Ap Sequence 75288, Ap Sequence 62362, A Sequence 62362, A Sequence 83439, A Sequence 37439, A Sequence 84672, Sequence 84672, Sequence 73, Appl

Sequence 95035, Sequence 62485, A Sequence 62485, A Sequence 263451, Sequence 263452, Sequence 404802, Sequence 210331, Sequence 210331,

Sequence 199, App

Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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Sequence 1, Application US/10522789
Publication No. US20050260732A1
GENERAL INFORMATION:
APPLICANT: TANABE SETYAKU CO., LTD.
TITLE OF INVENTION: Thee-dimensional structure of dipeptidyl peptidase IV
FILE REFERENCE: 03-039-PCT
CURRENT APPLICATION NUMBER: US/10/522,789
CURRENT PILING DATE: 2005-01-28
PRIOR PILING DATE: 2005-01-29
PRIOR FILING DATE: 2002-07-29
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Version 3.1
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC 174
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6 US-09-925-065A-857835

6 US-09-925-065A-474460

8 US-10-750-623-62484

12 US-11-136-527-6312

12 US-11-136-527-6314

12 US-11-136-527-6316

13 US-11-136-527-6316

14 US-11-136-527-6316

15 US-09-925-065A-952885

16 US-10-750-185-62362

17 US-11-121-086-73

18 US-10-750-185-62453

18 US-10-750-185-62485

18 US-10-750-185-62485

18 US-10-750-185-62485

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18 US-09-925-065A-263452
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1271
1271
574
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; OTHER INFORMATION:
US-10-522-789-1
     NAME/KEY: CDS
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Sequence 168, App
Sequence 164, App
Sequence 71343, A
Sequence 71343, A
Sequence 892716, Ap
Sequence 866910,
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Sequence 19, Appl
Sequence 396, App
Sequence 4038, App
Sequence 4038, App
Sequence 546409,
Sequence 735709,
Sequence 735709,
Sequence 5, Appli
Sequence 16709,
Sequence 956, App
                                                                                                           February 17, 2006, 05:06:42; Search time 654 Seconds (without alignments) 7088.778 Million cell updates/sec
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                  GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-186-284-54
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US-09-925-065A-899711
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US-09-925-065A-899711
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241 AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATTGACATTTATGATTTAAAT 300 355 AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCCATATGACATTTATGATTTAAAT 414 301 AAAAGGCAGCTGATTACAGAAGAGGATTCCAAACACACAC	AATTTACCAAGTTACAGAATCACATGGACGGGAAAGAGATATAATATATAATGGAATA AATTTACCAAGTTACAGAATCACATGGACGGGGAAAGAGATATAATATATAT	AACGG TCCTT TCCT TCCTT TCCTT TCC	THE STANCE TO CALLACTE ACTOR TO THE THE STANDARD STANDARD AND THE STANDARD	CCTTCAGAACCTCATTTACCCTTGATGGTAATACTCTCTACAGATCATCAGAATGAACCAACAATGAATCAATACTCTCTACAGAATCATCAGAATGAAT	
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NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2130
LENGTH: 4852
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Best Local Similarity 84.7%;
Matches 1850; Conservative 1
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; ORGANISM: Rattus norvegicus
US-11-136-527-2130
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TACAGAAGAGGATTCCAAACAACACACAGTGGGTCACATGGTCACCAGTGGGTCATAA
                               <u> Aagakgaaatrgagctriccrccrccaarrcagtarrrangcriggricgccrgtrigggagtaa</u>
                                                                  ATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCAAATTTACCAAGTTA
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                                                                                                                                                                                                                                                                                                Sequence 168, Application US/11245147

Sequence 168, Application US/11245147

Publication No. US20060030541A1

GENERAL INFORMATION:

APPLICANT: GARCIA, TERESA

APPLICANT: BARON, ROLAND

APPLICANT: CALL, KATHERINE

APPLICANT: THEILHABER, JOACHIM

APPLICANT: CALL, KATHERINE

APPLICANT: THEILHABER, JOACHIM

APPLICANT: CALL, KATHERINE

APPLICANT: CALL, KATHERINE

APPLICANT: CALL, KATHERINE

APPLICANT: GANGOLIY, THOTHY

APPLICANT: GEORGES

TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE

FILE REPERROR: 37991-0023

CURRENT PILING DATE: 2005-04-05

PRIOR APPLICATION NUMBER: ECT/1802/02211

PRIOR APPLICATION NUMBER: 60/281,400

PRIOR FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 246

SOFTWARE PARCHIN VET: 3.2

SEQ ID NO 168

SEQ ID NO 168

SEQ ID NO 168
                                                                       CAGATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGAT
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OTHER INFORMATION: Homo sapiens fibroblast activation protein, alpha
OTHER INFORMATION: (FAP), mRNA
US-11-245-147-168
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Pred. No. 1.3e-170;
0; Mismatches 825;
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Best Local Similarity 60.9%;
Matches 1320; Conservative
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334 CACACTGAAGGATATTTTAAATGGAACATTTTCTTATAAAACATTTTTTCCAAACTGGAT 393
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                   CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US10()301,822
PRIOR PILING DATE: 2002-11-21
PRIOR PILING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PRILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 784584
    CURRENT APPLICATION NUMBER: US/11/186,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.9
Matches 1320; Conservative
                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (209)...(2491)
US-11-186-284-54
                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
FEATURE:
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Buillemette, Tracy L.
APPLICANT: Kamatkar, Stubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John B.
APPLICANT: Thibodeau, Stephen B.
APPLICANT: Hibodeau, Stephen B.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
ACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTCTCAGACTGAA 1571
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PRILING DATE: 2000-11-30
PRIOR PRILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
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Pred. No. 1.9e-14;
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; Sequence 866910, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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Best Local Similarity 99.0%;
Matches 102; Conservative
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US-09-925-065A-899711
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US-09-925-065A-899711/c
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Pred. No. 1.6e-16;
0; Mismatches 528; Indels
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                                                          Sequence 2716, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Probe Arrays For Express
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SEQ ID NO 2716
SEQ ID NO 2716
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US-11-136-527-2716
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Matches 479; Conservative
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PRIOR FILING DATE: 2000-08-21
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US-11-151-601-19
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR SEQ ID NOS: 957066
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 866910
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APPLICANT: Mayers, Rachel E.
APPLICANT: Olandt, Peter J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Worker HUMAN PROTEIN KINASE, PHOSPHATASE,
ITILE OF INVENTION: NOVE HUMAN PROTEASE FAMILY
FILE REFERENCE: MPTOO-054PIRCPLOMIDUM
CURRENT APPLICATION NUMBER: US 10/170, 789
PRIOR PILING DATE: 2002-06-13
PRIOR PLING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
PRIOR PLING DATE: 2001-02-28
PRIOR PLING DATE: 2001-06-15
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PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/934,406
PRIOR PLING DATE: 2001-06-15
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98.1%; Pred. No. 2.3e-14;
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Publication No. US20060003413A1
GENERAL INFORMATION:
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-866910
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2417 CAAATCGTTTACTGCTCTTACATGGTTTCCTGGATGAGAATGTCCATTTTGCACATACCA 2476
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APPLICANT: Milennium Pharmaceuticals, Inc.,
APPLICANT: Meyers, Rachel E.
APPLICANT: Olandt, Peter J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: MPIO0-054PLRCP10MIDVIM
CURRENT APPLICATION NUMBER: US 10/170,789
PRIOR APPLICATION NUMBER: US 90/797,039
PRIOR PILING DATE: 2002-06-13
PRIOR PILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: PCT/US01/06525
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2649
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                                                                                                                                                                                                                                                                                                      3.6%; Score 77.8; DB 12;
48.7%; Pred. No. 1.7e-08;
ative 0; Mismatches 252;
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Publication No. US20060003413A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.7°
Matches 242; Conservative
                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-151-601-21
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APPLICANT: Hann, Louane B.
APPLICANT: Sinacore, Martin S.
APPLICANT: Sinacore, Martin S.
APPLICANT: Sinacore, Martin S.
APPLICANT: Broam, Mark W.
APPLICANT: Brown, Bugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REPRENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT APPLICATION NUMBER: US/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PATENTIN VETSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1945 ACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAACA 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70.4; DB 12; Length 379; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4038, Application US/11128061; Publication No. US20060003958A1; GENERAL INFORMATION:
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                                        Charlebois, Timothy S. Mounts, William M.
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Best Local Similarity 92.5%;
Matcheë 74; Conservative
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; ORGANISM: Cricetulus griseus
US-11-128-061-396
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                 Melville, Mark W.
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Best Local Similarity
Matches 74; Conserv
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PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR PILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 90/882,166
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/212,078
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/934,406
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2001-08-21
PRIOR PLING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 3143
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US-11-128-061-396
US-11-128-061-396, Application US/11128061
Publication No. US20060003958A1
GENERAL INFORMATION:
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Matches 242; Conservative
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; LOCATION: (229)...(2874)
US-11-151-601-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Hann, Louane E.
APPLICANT: Sinacore, Mark M.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDE RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
TITLE OF INVENTION NUMBER: US/11/128,061
CURRENT APPLICATION NUMBER: US/11/128,061
PRIOR PAPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
SEQ ID NO 4038
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Pred. No. 4.4e-07;
0; Mismatches 6;
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1752 ACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGGTCCTGGGATC 1811
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                                                                                                                                                                                                    1945 ACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTTGAGTACCTCCTTATTCATGGAACA 2004
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                                                                                                                                                                                                                                                                                            2 acadrcardadecadadergaaaarrrraaacaagrrcagraccrccrrarrcarddaaca
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1S-equence 546409/C

1Sequence 546409/Application US/09925065A

1S-equence 546409/Application US/09925065A

1S-equence 546409/C

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Score 70.4; DB 12; Length 379;
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0; Mismatches 6; Indels 0
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Sequence 4038, Application US/11128049

Sequence 4038, Application US/20060010513A1

GENERAL INFORMATION:

APPLICANT: Malville, Mark W.

APPLICANT: Charlebois, Timothy S.

APPLICANT: Hann, Louane E.

APPLICANT: Brown, Bugene L.

APPLICANT: Brown, Eugene L.

APPLICANT: Bugene L.

APPLICANT: Bugene L.

APPLICANT: Bugene L.

APPLICANT: Bugene L.

APPLICANT: Miller, Christopher P.

APPLICANT: Miller, Christopher P.

APPLICANT: Miller, Christopher P.

APPLICANT: Muller, Christopher P.

APPLICANT: Muller, Christopher P.

APPLICANT: WARRIG AND USING SAME

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

TITLE OF INVENTION: UNABER: US 60/570,425

FRIOR APPLICATION NUMBER: US 60/570,425

PRIOR APPLICATION NUMBER: US 60/570,425

PRIOR APPLICATION NUMBER: SO04-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PRECENTING ABBERNIEL NUMBER: US 60/570,425

MUNDER OF SEQ ID NOS: 7285

SEQ ID NO 4038

LENGRIH: 379
                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION NO. US.2000010313A1

APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Brown, Eugene L.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
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Publication No. US20060010513A1
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Sequence 5, Appli
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Sequence 63, Appl
Sequence 613, Appl
Sequence 4170, Ap
Sequence 125, Appl
Sequence 1371, Ap
                                                                                                                                                                      February 17, 2006, 05:01:13; Search time 1790 Seconds (without alignments) 10089.565 Million cell updates/sec
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24	751	•	2814	m	-09-954-456-11	Sequence	1148, Ap	Q,
25		٠.	2814	m	-09-954-531-367	Sequence	367, App	Ω
56		34.4	2814		US-09-873-367C-499	Sequence	499, Ap	Ω
27		٠.	2814		US-10-177-293-135	Sequence	135, Ap	Ω
28			2814		US-10-101-510-30	Sequence	30, App	_
50		34.4	2814		US-10-301-822-54	Sequence	54, Appl	-
30		4.4	2814		US-10-240-425-1414	Sequence	1414, A	ο.
1 C		4.4	4187		US-IU-4/3-9/4-I68	Sequence	168, Ap	Ω. (
2 6		3.4.4 4.4	2814		US-10-843-641A-439 IIS-10-843-6418-1434	Sequence	477, AD	ο, α
) E		4.4	2814		US-10-843-641A-4175	Seguence	4175	D. C
35		34.4	2814		US-10-843-641A-5994	Sequence	5994. A). C
36		34.4	2814		US-10-884-070A-6	Seguence	6. Appl	
37		34.4	2815		US-09-265-606-1	Sequence	1, Appli	•=
38		34.4	3224		US-10-240-965-117	Sequence	117, Ap	0.
39		33.0	2812		US-10-084-817-24	Sequence	24, App	_
40	216	23.6	529		US-09-878-178-2021	Seguence	2021, A	O ₄
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7 7	010	6.50	770	n n	US-10-146-502-2021	Sequence	2021,	ο, (
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45	511.8	23.4	533	n n	US-10-146-502-2043	Sequence	2043, Ap	ο, ο,
					ALIGNMENTS			
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US-10-0	-10-002-593-5	;			!			
; Seque ; Publi	Sequence 5, Application US/1000259 Publication No. US20020137120Al	pplicat o. US20	10n US/ 0201371	20A	02593 1			
O	GENERAL INFORMATION: APPLICANT: Vanderhi	MATION:	lt Imiv	7	-			
	APPLICANT: Brown, Nancy J.	Brown, Nancy J	Nancy J	. i	K 3 1			
	E OF INV	ENTION:	BIOLOG	S E	TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERT:	TOR ASSOCT	GIOTENS	IN CONVERT
	REFEREN	CE: Att)	y Docke	Ž	o. US20020137120A1 1242/48	/2		
	CURRENT APPLICATION N	ICATION	NUMBER: US/	. T	S/10/002,593 -31			
	PRIOR APPLICATION NUMBER: 60/244,5	ATION M	JMBER:	209	244,524			
	NR FILING	DATE	2000-10	-31				
SOFT	SOFTWARE: Patentin version	tentin	s: 10 version	w.	т			
; SEQ 1	SEQ ID NO 5 LENGTH: 3407	,						
; TYP ; ORG US-10-0	TYPE: DNA ORGANISM: Homo sapiens -10-002-593-5	ото вар:	iens					
Query	Query Match	:	100.08;	*0.	Score 2184; DB 5;	Length 3407;		
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241 AACTACGTGAAGCAATGGAGGCATTCCTACACACTTCATATGACATTTATAAAT AACTACGTGAAGCAATTGGAGGCATTCCTACAGCTTCATATGACATTTATGATTTAAAT

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TGCTTAGTGGCACGGCAACACATTGAAATGAGTACTACTGGCTGG	1021 GAAGSTRAGAGCAATTIGCTATTICCAATRAGATAAAAGACTGCAATTATTACA 108 1210 GAAGGTTACAGACACATTIGCTATTITCCAAATAGATAAAAAGACTGCACATTTATTACA 126 1081 AAAGGCACCTGGGGAAGTCATCGGGAATAGAGATAAAAAGACTGCACATTATTACA 126	AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT	AGTAATGAATATAAAGGAATGCCAGGAGGAATCTTTATAAAATCCAACTTATTGAC 	TATACAAAGTGACTGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT 	GIGICATICAGIPAAGAGGCGAAGIATTAICAGCIGAGATGITCGGGICCIGGICTGCCCCCCCAGICATAGAAGGGCGAAGIATTAICAGCIGAGATGTTCGGGICCIGGICTGCCCCGGICAGAAGAAGAAGAATGAACAAGAATGTTCGGGICCIGGGICTGCCGCTGCCCGGICCAGGAAGAAGAAGAAAGAAAGAAAGAAAGAAA	CTCTATACTCTACACACCACCAATGATAAAGGGCTGAGAGTCCTGGAAGACAATTCA 	GCTTTGGATAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT 	TTGAATGAAGAAATTTGGTATCAGATGATCTTGCCTCGTTTTGATAATCCAAG 	AAATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAGCAGACAGTCTCTCTTCTTTTTTTT	TTCAGACTGAACTGGGCCACTTACCTTGCAAGACACAAAACATTATAGTAGCTAGC	GATGGCAGAGGAAGTGGTTACCAAGGAGATAAGATCATGCATG	GGAACATTIGAAGITGAAGITGAATTGAAGGAGCAGCAAGCAAGTTITCAAAAATGGGATTT GGAACATTIGAAGITGAAGATCAAATTGAAGCAGCAGACAATTTICAAAAATGGGATTT	GIGGACAACGAACTIGCAATTIGGGGCTGGTCATAIGGAGGGTACGTAACCTCAATG 			1921 AACCTTGACGATTACGAGAATTCGACGAGGGGGGGGGGG
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6 LENGTH: 3407 TYPE: DNA ORGANISM: Homo sapiens FRATURE: NAME/KEY: CDS LOCATION: (76)(2376)	Query Match 100.0%; Score 2184; DB 5; Length 3407; Best Local Similarity 100.0%; Pred. No. 0; Matches 2184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC 60 	61 TCCTTAAGATGTTTCAGATCATGAATATCTCTACAACAAGAAATAATATCTTGGTA 120 	121 TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT 180 	181 GGACATICTATCAATATICAATATCTCCTGATGGGCAGTITATICTCTTAGAATAC 240 	241 AACTAGGGGAAGGGGATTCCTACACAGCTTCATATGACATTTATGATTTAAAT 300 	301 AAAAGGCAGCTGATTACAGAAGAGGAGTTCCAAACAACACACAC	361 CCAGTGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCA 420 	421 AATTTACCAAGTTACAGAATCACATGGACGGGAAAGAAGATATAATATAATGGAATA 480 	481 ACTGACTGGGTTTATGAAGAGAAGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTGTCCA 540	541 AACGGCACTTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC 600 	601 TCCTTCTACTCTGATGAGTCACTGCAGAAGACTGTACGGGTTCCCATATCCAAAG 660 	661 GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTAGAAATACAGACTCTCTCAGCTCA 720 	121 GTCACCAATGCAACTTCCATACAAATCACTGCTCCTGCTTCTATGTTGATGGGGGATCAC 780	181 TACTIGIGATGIGACAIGGGCACACAGAAAGAATTICTTIGCAGIGGCTCAGGAGG 840 	841 ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAAC 900
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48 ACTOACCHOGTTANGAGAATCACANGACAAAACAACAACAACAACAACAACAACACAAAATCACAAATCACAAAACAAAAACAAAACAAAACAAAATCACAAAAACAAAAACAAAATCACTACAAAAACAAAAATCAATTAAACAAAAACAAAATCATTAAAACAAAAAA
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PRIOR PILING DATE: 2001-11-21
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PRIOR PLING DATE: 2001-12-14
PRIOR PLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-10
PRIOR PLILING DATE: 2002-01-10
PRIOR PLILING DATE: 2002-01-18
PRIOR PLILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR PRIOR DATE: 2002-02-03
PRIOR PRIOR DATE: 2002-02-03
PRIOR PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PRIOR DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 921
TENDATH: 3407
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190 TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG
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US-10-295-027-921
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APPLICANT: Afar, Daniel
APPLICANT: Afar, Daniel
APPLICANT: Glaberg, Wendy M.
APPLICANT: Glab, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Markon, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Worders: 2002-11-13
PRIOR PELICATION NUMBER: US 09/663,733
PRIOR PELICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
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                                        GGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCAGACAATTTTCAAAAATGGGATTT
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Publication No. US20030232350A1
GENERAL INFORMATION:
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AAAAGGCAGCTGATTACAGAAGAGAGTTCCAAACAACAACACACAGGGGTCACATGGTCA 54 CCAGTGGGTCATAAATTGACATAGGATTCGAACAATGACATTAATGTTAAAATTGAACCA 42 CCAGTGGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTAATGTTAAAATTGAACCA 60 AATTTACCAAGTTACAAGATCACATGGACGGGAAAGAAGATATAATAATAAAATTGAATA 66 AATTTACCAAGTTACAAGAATCACATGGACGGGGAAAGAAGAATAAATA	670 ACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGGTGGTGGTCTCCA 729 541 AACGGCACTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC 600 130 AACGGCACTTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC 789 601 TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG 660 790 TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG 849 661 GCAGGAGGTGCATGAATGATCAATTGTTGTAAAAAACTTCTTCAAAGTCCTCAAGTCA 720 61 GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTAAATACAGACTCTCTCAACTCA 720 850 GCAGGAGCTGTGAATCCAACTGTAAAAGTTCTTTGTTAAATACAGACTCTCTCAACTCA 720 850 GCAGGAGCTGTGAATCCAACTGTAAAAGTTCTTTTTTTTT		1090 TGCTTAGTGGCACGCAACACTTGAATGAGTACTACTGGCTGG	

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kochan, Jarema Peter;
APPLICANT: Mochan, Jarema Peter;
APPLICANT: Mosinski, James Andrew;
TITLE OF INVENTION: Specific Markers for Dia;
FILE REFERENCE: 21270US1;
CURRENT APPLICATION NUMBER: US/10/952,459;
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 17.
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| Sequence 216, Application US/10887553A
| Publication No. US20050085436A1
| GENERAL INFORMATION:
| APPLICANT: Garza, Dan
| APPLICANT: Li, Hao
| TITLE OF INVENTION: With insulin signalling dysregulation
| TITLE OF INVENTION: with insulin signalling dysregulation
| TITLE OF INVENTION: with insulin signalling dysregulation
| FILE REFERENCE: 4-33262
| CURRENT APPLICATION NUMBER: US/10/887, S53A
| CURRENT FILING DATE: 2004-09-06
| PRIOR PILING DATE: 2003-08-07
| NUMBER OF SEQ ID NOS: 1208
| SOFTWARE: RastSEQ for Windows Version 4.0
| SEQ ID NO 216
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                                                                                                                                                                                               Score 2180.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                    NO: 1026
            INFORMATION FOR SEQ ID NO: 1026:
SEQUENCE CHARACTERISTICS:
LENGTH: 2924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                    LIBRARY: GENBANK
CLONE: 9180082
SEQUENCE DESCRIPTION: SEQ ID
US-10-641-643-1026
 (650) 845-4166
                                                                                                                                                                                                99.94;
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Best Local Similarity 99.9
Matches 2182; Conservative
 TELEFAX:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: Ploppy disk
COMPUTER: DE Compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWN>
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CORRESSENDINGES: ADDRESSES
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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REGISTRATION NUMBER: 37,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR
GENE EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1026, Application US/10641643
Publication No. US:20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
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ATTORNEY/AGENT INFORMATION:
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    ACAAAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTAC
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CTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012789
US-09-917-800A-1570
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PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR PAPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PATENTING VET: 2.1
SEQ ID NO 1570
LENGTH: 4835
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		CTGGGAACATTGAAGTTGAAGATGAAGCAGCCAGACAATTTTCAAAAATGGGA 1 [
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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8: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	qı	US-10-002-593-5	US-09-949-016-275	US-10-423-714-5	US-09-949-016-4579	US-09-023-655-1026	PCT-US93-07923-1	US-08-230-491A-1	US-08-619-280A-1	US-08-940-391-1	US-09-265-606-1	US-09-949-016-2459	US-09-389-681-428	US-09-620-405B-428	US-09-433-826B-428	US-09-604-287A-428	US-09-834-759-428	US-09-590-751A-428	US-09-551-621-428	US-09-551-621A-428	US-10-076-622-428	US-10-363-937-21	US-09-976-674-6	US-09-976-674-42	US-09-949-016-12017
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Sequence 16321, A	Sequence 44, Appl	Sequence 32, Appl	Sequence 13726, A	Sequence 23690, A	Sequence 163433,	Sequence 646, App	Sequence 1, Appli	Sequence 1, Appli	S	Sequence 1, Appli	Sequence 1, Appli	1,	Sequence 249, App	Sequence 2, Appli	Sequence 1103, Ap	Sequence 2, Appli	Sequence 14, Appl	Sequence 22, Appl	Sequence 12, Appl	Sequence 14201, A
US-09-949-016-16321	US-09-976-674-44	US-09-392-184-32	US-09-270-767-13726	US-09-949-016-23690	US-09-949-016-163433	US-09-221-017B-646	US-09-079-592-1	US-09-462-284-1	US-09-248-796A-5369	US-08-699-103B-1	US-09-229-059-1	US-09-628-133-1	US-09-280-116-249	US-09-976-674-2	US-09-976-594-1103	US-10-070-464-2	US-09-976-674-14	US-09-976-674-22	US-09-976-674-12	US-09-949-016-14201
85878 3	496 3	239 3	1023 3	601 3	601 3	657 3	280 3	5496 3	.485 3	1982 3	982 3	982 3	547 3	671 3	2797 3	120 3	309 3	4685 3	4829 3	6848 3
9.0 85	8.1	6.5	5.6	5.0	2.0	4.5	4.2		_	_	_				3.6			3.6		_
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RESULT 1 US-10-002-593-5 Sequence 5, A PARENT INFORM: APPLICANT: TITLE OF INV. TYPE: DNA CRGANISM: H	SULT 1 -10-002-593-5 Sequence 5, Application US/10002593 Patent No. 6586198 GENERAL INFORMATION: APPLICANT: Brown, Mancy J. APPLICANT: Brown, Mancy J. ITILE OF INVENTION: INHIBITOR AND VASOPEPTIDASE INHIBITOR ASSOCIATED ANGIOEDEMA TITLE OF INVENTION: INMIRER: US/10/002,593 CURRENT APPLICATION NUMBER: US/10/002,593 CURRENT FILING DATE: 2000-10-31 PRIOR APPLICATION NUMBER: 60/244,524 PRIOR APPLICATION NUMBER: 60/244,524 PRIOR APPLICATION NUMBER: 60/244,524 PRIOR APPLICATION NUMBER: 00/244,524 RIGHT APPLICATION NUMBER: 00/244,524 PRIOR APPLICATI
Query Match Best Local Sim Matches 2184;	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy Db	1 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATAC 60
Oy 63	61 TCCTTAAGATGGATTTCAGATCATGAATATCTCTACAACAAGAAAATAATATCTTGGTA 120
Qy 12	121 TICAANGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT 180
2y 18	181 GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC 240
Qy 24	241 AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAAT 300
97	301 AAAAGGCAGCTGATTACAGAAGAGAGTTCCAAACAACACACAGTGGGTCACATGGTCA 360

1519 GCTITGGATAMANTGCTCCAGANTGCCCTCCAAAAACTGGACTTCATTATT 1629 1441 TIGANTGAACAAATTTTGGTACTGATTCCTCCTCCTATTTTGATAAACCAG 1500 1501 AAATATCTACAAAATTTTGGTACTGATTCCTCCTCCTATTTTGATAAACCAG 1500 1502 AAATATCTCACAAAATTTTGGTACTGATTCCTCCTCCTATTTTTGATAAACCAG 1689 1503 TIGAACCAAAAAATTTTGGTACTGAAGACCCCATGTACTAAAACCAACACTGTC 1560 1504 AAATATCTCAAAATTTTGGTACTGAAGACCCCATGTACAAAAAACAAAAACAACAACAACAAAAACAAAAACAAAA	sequence 275, Application US/09949016 Sequence 275, Application US/09949016 Parent No. 6812339 GENERAL INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT FILING DATE: 2000-04-1/35 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 NUMBER OF SEQ ID NOS: 207012
	1389 1260 1449 1320 1509 1380

1090 961 1150	1021	Qy 1081 AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT 1140 Db	QY 1141 AGTAATGAATATAAAGGAATGCCAGGAGGAATCTTTATAAAATCCAACTTATTGAC 1200	OY 1201 TATACAAAGTGACATGCCTCAGTTGTGAGCTGGAATCCGGAAAGGTGTCAGTACTATTCT 1260	Qy 1261 GTGTCATTCAGTAAAGAGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC 1320	QY 1321 CTCTATACTCTACACAGCGGGAATGATAAAGGGCTGAGAGTCCTGGAAGACAATTCA 1380 DD	OY 1381 GCTTTGGATAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT 1440 1570 GCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT 1629	Qy 1441 TTGAATGAAACAAAATTTTGGTATCAGATCATCTTGCCTCCTCATTTTGATAAATCCAAG 1500 DD 1630 TTGAATGAAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAG 1689	Oy 1501 AAATATCCTCTACTATAGATGTGTATGCAGGCCCATGTAGTAAAAGGAGAGACACTGTC 1560	Oy 1561 TICAGACTGAACTGGGCCACTTACCTTGCAAGCACAGAAACATTATAGTAGCTAGC	Oy 1621 GATGGCAGAGGAGAGTCTACCAAGGAGATAAGATCATGCATG	OY 1681 GGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTTCAAAAATGGGATTT 174	OY 1741 GTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACGTCAATG 180	OY 1801 GTCCTGGGAACGGGAGTGTCAAGTGTGGAATAGCCGTGGCCTGTGTCCCGG 1860	Qy 1861 TGGGAGTACTATGACTCAGTGTACACAGAACGTTACATGGGTCTCCCCAACTCCAGAAGAC 1920 Db 2050 TGGGAGTACTATGACTCAGTGTACACAGAACGTTACATGGGTCTCCCCAACTCCAGAAGAC 2109	dy 1921 AACCTTGACCATTACAGAAATTCAACAGTCATGAGCAGGCTGAAAATTTTAAACAAGTT 198 Db 2110 AACCTTGACCATTACAGAAATTCAACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTT 216	Oy 1981 GAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCAG 204 Db 2170 GAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCAG 222
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 275 LENGTH: 3407 LYPE: DNA ORGANISM: Human S-09-949-016-275	Query Match 100.0%; Score 2184; DB 3; Length 3407; Best Local Similarity 100.0%; Pred. No. 0; Matches 2184; Conservative 0; Mismatches 0; Indels 0; Gare 0;	CTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGT 		AGTTT AGTTT	U 4	TAAAT 3 TAAAT 4	661CA		AAITTRACCAAGTTACAGAATCACATGGACGGGGAAAGAAGATATAATATAATGGAATA 	ACTGACTGGGTTTATGAGGGGAGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTCTCCA	AACGGCACTITITAGCATATGCCCAATTAACGACACAGAAGTCCCACTTATTGAATAC	TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG	GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA 	GTCACCAATGCAACTTCCATACAATCACTGCTCCTGCTTCTATGTTGATAGGGGATCAC			TAGG

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Facett No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,756
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4579
LENGTH: 3419
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 2183; Conservative C
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US-09-949-016-4579
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US-09-949-016-4579
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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                                                                                                                                  APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DET
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALL ALTO
STATE: CALIFORNIA
COUNTRY: USA
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99.9%; Pred. No. 0;
ive 0; Mismatches
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ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0556
INFORMATION FOR SEQ ID NO: 1026:
SEQUENCE CHARACTERISTICS:
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                                  RESULT 5
US-09-023-655-1026
Sequence 1026, Application US/09023655
Perent No. 6607879
GENERAL INFORMATION:
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Matches 2182, Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                             GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAAATACAGACTCTCTCAGCTCA
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                             TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 502 or 553X
COMPUTER: 18M PS/2 Model 502 or 553X
OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07923
FILING DATE: 19930819
CLASSIFICATION NUMBER: 07/934,162
PRIOR APPLICATION NUMBER: 07/934,162
PRIOR APPLICATION NUMBER: 07/932,211
PRING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/055002
TELECOMMUNICATION INFORMATION:
TELECHOME (677) 542-5700
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TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07923-1
                                                                                                                                                                                                                                                                                                                                               LENGTH: 2924
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2815 Base pairs
; TYPR: nucleic acid
; STRANDEDNESS: double
; TOPOLLGY: linear
US-08-230-491A-1
                                                                                                                                                                                                    Best Local Similarity 60.9 Matches 1320; Conservative
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Patent No. 5587299
GENERAL INFORMATION:
APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;
APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STORAGE
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MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB f
COMPUTER: IBM P6/2
OPERATING SYSTEM: PC-DOS
SOFTWARES: WORDERRECT - ASC II
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/230,491A
PILING DATE: 20-APRIL-1994
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ATTORNEY/AGENT INFORMATION:
NAME: HARBON, NO. 5587299man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
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STREET: 805 THIRD AVENUE
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CITY: NEW YORK
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US-08-230-491A-1
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COUNTRY:
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                    CCTGGTCGATGTTGGAGTGGATTTTCCAGGCAATGTGGTATACTGATGAAGACCATGGAAT
                                             AGCTAGCAGCACACACACATATATATACCCACATGAGCCACTTCATAAAACAATG
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                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Zimmermann, Rainer; Park, John B.;
APPLICANT: Rettig, Wolfgang; Old, Liloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
TITLE OF INVENTION: ALPHA, AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB
COMPUTER: IBM PS/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280A
FILING DATE: 18-MARCH-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 5767242man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 1UD 5330.
TELECOMUNICATION INFORMATION:
TELEPACN: (212) 688-9200
TELEPAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATTERISTICS:
LENGTH: 2815 Base pairs
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08619280A
Patent No. 5767242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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Matches 1320; Conservative
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STRANDEDNESS: double
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SOFTWARE: Wordper
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US-08-619-280A-1
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GGAGCATATAGAAGAAAGCAGAACTGGATGGGCTGGTGGATTCTTTGTTTCAAGACCAGT
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                                           TTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAAGAAGGTTACAGACA
                                                                                 TTTCAGCTATGATGCCATTTCGTACTACAAAATATTTAGTGACAAGGATGGCTACAAACA
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                                               ACACAGCAGCGTGAATGATAAAGGGCTGAGAGTCCTGGAAGACAATTCAGCTTTGGATAA
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APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION
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TITLE OF INVENTION: PROTEIN ALPHA, AND USES THEREOF NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: 4 Lynch
STREET: 805 Third & Lynch
STREET: 805 Third Avenue
CITY: New York
CUTY: New York
CONTYRY: USA
ZIP: 1002A
ZIP: 1002A
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.4%; Score 751; DB 2; Lu
Best Local Similarity 60.9%; Pred. No. 1e-218;
Matches 1320; Conservative 0; Mismatches 825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, No. 596373man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5330.1
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 888-9200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2815 Base pairs
                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 2.0 COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,391
FILING DATE: 01-0CT-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/619,280
FILING DATE: 18-MARCH-1996
APPLICATION NUMBER: 08/230,491
FILING DATE: 20-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: HARBON, NO. 5965373man D.
                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-940-391-1
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                                                                                                                                                                                                                                                                                                                                                                Length 2815
                                                                                                                                                                                                                                                                                                                                                          34.4%; Score 751; DB 3; Length 28 60.9%; Pred. No. 1e-218; ive 0; Mismatches 825; Indels
                APPLICATION NUMBER: 08/290,491
FILING DATE: 20-ARRIL-1994
ATTONNEY, AGENT INFORMATION:
NAME: Hanson, No. 6846910man D.
REGISTRATION NUMBER: 30,946
REPREMENCE/DOCKET NUMBER: LUD 5330.1
TELECHONE: (212) 688-9200.
                                                                                                                                                                     INFORMATION FOR SEQ 10 SB8-3884
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2815 Base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    18-MARCH-1996
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.9
Matches 1320; Conservative
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
  FILING DATE:
                                                                                                                                                                                                                                                                                                                       US-09-265-606-1
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                                                                                                             1936 AACAGCTTTCCAAGGTGAACTCCTCTATGCAGTGTATCGAAAGCTGGGTGTTTATGA
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  AAGTGGTTACCAAGGAGATAAGATCATGCAATCAACAGAAGACTGGGAACATTTGA
                                                                                                                                                          AGTTGAAGATCAAATTGAAGCAGCCAGACAATTTTCAAAAATGGGATTTGTGGACAACAA
                                                                                                                                                                                               1996 AGTIGAAGACCAGAITACAGCIGICAGAAATICATAGAAATGGGITICATIGAIGAAA
                                                                                                                                                                                                                                       ACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATGGTCCTGGGATC
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Patent No. 6846910
GENERAL INFORMATION:
APPLICANT: Zimmermann, Rainer; Park, John E.;
APPLICANT: Rettig, Wolfgang; Old, Lloyd J.
ITILE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROT;
ITILE OF INVENTION: ALPHA, AND USES THEREOF
OORRESPONDENCES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York City
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/619,280
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APPLICATION NUMBER: US/09/265,606
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY...
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPR: Diskette, 3.5
MENTER: IBM PS/2
PC-DOS
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OPERATING SYSTEM: PC-DOS
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Sequence 2459, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: To Craig et al. |
| GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT PILLING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-3 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
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AGCTAGCAGCACACCACCAACATATATATACCCACATGAGCCACTTCATAAAACAATG
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30.7%; Score 669.4; DB 3;
Best Local Similarity 59.6%; Pred. No. 9.5e-194;
Matches 1296; Conservative 0; Mismatches 801;
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; ORGANISM: Human
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                                                 .096 CACGTGGGTTACTGATGAAGGAGTATGTTTGCAGTGGCTAAAAAGAGTCCAGAATGTTTC 1155
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                                                                                                                                                                                                                                                                               TTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAAGAAGGTTACAGACA
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       GACATGGGCAACAAGAAAGAATTTCTTTGCAGTGGCTCAGGAGGATTCAGAACTATTC
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Sequence 428, Application US/09389681A
| Patent No. 651827
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Yuqui, Jiang
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Mitcham, Jennifer L.
| TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
| TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
| FILE REFERENCE: 210121.470C3
| CURRENT FILING DATE: 1999-09-02
| CURRENT FILING DATE: 1999-09-02
| WINDER OF SEQ ID NOS: 463
| SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Jiang, Yuqui
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REPRENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433,826B
CURRENT APPLICATION NUMBER: US/09/433,826B
NUMBER OF SEQ ID NOS: 474
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Pred. No. 2.3e-70;
0; Mismatches 167;
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Patent No. 6579973
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqui
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US-09-433-826B-428
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Best Local Similarity
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US-09-433-826B-428
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Sequence 428, Application US/09620405B

Patent No. 6528054

GENERAL INFORMATION:

APPLICANT: Jiang, Yuqiu

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.470C8

CURRENT APPLICATION NUMBER: US/09/620,405B

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 495

SOFTWARE: FRAESEQ for Windows Version 3.0
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Pred. No. 2.3e-70;
0; Mismatches 167;
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                              GGGGCTGGTCATATGGAGGGTACGTAACCTCAATGGTCCTGGGATCGGGAAGTGGCGTGT
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| Patent No. 658672
| GENERAL INFORMATION:
| APPLICANT: Jiang, Yuqiu
| APPLICANT: Jiang, Yuqiu
| APPLICANT: Mitcham, Jennifer L.
| APPLICANT: Wi, Jiangchun C.
| APPLICANT: Wi, Jiangchun C.
| APPLICANT: Halocker; Suean L.
| APPLICANT: Halocker; Suean L.
| APPLICANT: Halocker; Suean L.
| APPLICANT: Halocker; Suean L.
| APPLICANT: Milliam L.
| TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER |
| FILE REFERENCE: 210121.470C7 |
| CURRENT APPLICATION NUMBER: US/09/604,287A |
| CURRENT FILING DATE: 2000-06-22 |
| NUMBER OF SEQ ID NOS: 489 |
| SOFTWARE: FastSEC for Windows Version 3.0 |
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; ORGANISM: Homo sapiens
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February 17, 2006, 04:14:35; Search time 1316 Seconds (without alignments) 11060.554 Million cell updates/sec

US-10-659-055-2 2184 1 agtcgcaaaacttacactct......aacaatgtttctctttacct 2184 Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4996997 seqs, 3332346308 residues Searched:

9993994 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N_Geneseq_21:* 1: geneseqm1980s:* 2: geneseqm1990s:*

11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ado40239 Human DPP	Abk92227 Prostate	Aal44351 Human dip	Abz22557 Human liv	Add14640 Human src	Adn39603 Cancer/an	Ado19399 Human PRO	Adv25524 Human dip	Adn39271 Cancer/an	Adi83980 Human ful	-	-	Adj74790 Marker ge	Ado19397 Human PRO	Ado71613 Nucleotid	•	Adp54457 Human PRO	Adu06201 Novel bro	
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ADY15160	ADZ14037	AD248887	AEB94224	AAQ46089	ADL24801	ADI31700	ADO19805	AD071611	ADS83767	AAQ63261	ADQ80241	ADO71641	ACF87398	ADL24802	ADJ75717	AD071645	AEB94225	ABK63663	ABZ22556	ADB58114	ADB52598	ADP72568	ABZ35572	AEB94221	ADN95553
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6.66	6.66	6.66	6.66	6.66	99.9	6.66	6.66	6.66	99.9	8.66	7.66	99.4	99.4	9.94	76.8	76.8	76.8	75.8	75.8	75.8	75.8	75.8	34.5	34.5	34.5
2182.4	2182.4		2182.4	2180.8	~	2180.8	~	~	(1	.,	•		2170.4	1677.6	9.7791	_	-	165	1656.2	_	1656.2	1656.2	754.2	752.6	752.6
20	21	22	23	24	25	56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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crystal; mammalian dipeptidyl-peptidase IV extracellular domain; dipeptidyl-peptidase IV extracellular domain; DPP-IV extracellular domain; three-dimensional structure; antidiabetic; anorectic; cytostatic; type I diabetes; type II diabetes; cancer; human; DPP-IV; enzyme; gene; 88; protein co-ordinate data;
                                                                      Human DPP-IV extracellular domain encoding cDNA SEQ ID NO:1.
                 ADO40239 standard; cDNA; 2211 BP.
                                                     (first entry)
                                                     12-AUG-2004
                                                                                                                                    EC 3.4.14.5.
                                   ADO40239;
RESULT 1
ADO40239
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Homo sapiens.

/*tag= a /product= "DPP-IV extracellular domain" /BC_number= "3.4.14.5" Location/Qualifiers

EP1422293-A1.

26-MAY-2004.

17-NOV-2003; 2003EP-00026169.

25-NOV-2002; 2002EP-00026367.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

Thoma Hennig M, Loeffler BM,

Α,

WPI; 2004-413363/39. P-PSDB; ADO40240.

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New crystal of an extracellular domain of mammalian dipeptidyl-peptidase IV (DPP-IV) useful for identifying or designing inhibitors of DPP-IV

us-10-659-055-2.rng

The present invention describes a crystal (I) of the extracellular domain of mammalian dispetival-peptidase (DPP) 1.4 (S.) Also described:

(I) a co-crystal of the extracellular domain of mammalian DPP-IV and a ligand bound to its active site; (2) a co-crystal of the extracellular domain of mammalian DPP-IV and a ligand bound to its an algand to an allosteric binding of the mammalian DPP-IV and a ligand bound to mammalian DPP-IV and a ligand bound to mammalian DPP-IV and an active site ligand; (6) a co-crystal site in the extracellular domain of mammalian DPP-IV and an active site ligand; (6) a crystal produced by (MI) and (MI); (7) (7) determining the three-dimensional structure of a crystallisting an active site ligand; (6) a crystal produced by (MI) and (MI); (7) determining the three-dimensional structure of a crystallised extracellular domain of mammalian DPP-IV or a machine-readable data and active site being extractions for using the which, when using a machine programmed with instructions for using the data storage material encoded with machine readable data which, when using a graphical three-dimensional structure domain of mammalian DPP-IV comprising the ligand binding active site being defined by as set of points shaving a croom molecular complex comprising at least a portion of the extracellular domain continuate deviation of less than about 1.5 angstrom from points representation by using (I); (10) a pharmaceutical composition (II) and a carrier; (11) an isolated much set of sequence (SQC or mean square deviation the soluble extracellular domain of DPP-IV comprising (I) and a carrier; (11) an isolated much set of sequence (SQC of comprising (I); (10) a pharmaceutical composition; (11); and (12) a polypeptide comprising (I); (11) an isolate continue of sequence (SQC DNO:); (12) a polypeptide comprising (I); (11) an isolate of sequence (SQC DNO:); (12) a polypeptide comprising (I); (11) and a carrier; (11) an isolate of pop-IV activity, (I); is useful for the soluble extracellular domain of pop-IV ac Claim 26; SEQ ID NO 1; 215pp; English

Sequence 2211 BP; 716 A; 429 C; 466 G; 600 T; 0 U; 0 Other;

120 180 240 300 264 204 84 1 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATAC AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATAC 205 GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAAT AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAAT TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGAGTTT TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGATTTT GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC Gaps Query Match 100.0%; Score 2184; DB 12; Length 2211; Best Local Similarity 100.0%; Pred. No. 0; Marches 2184; Conservative 0; Mismatches 0; Indels 0; 25 61 121 145 241 181

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GCTTTGGATAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT 1440 1080 960 99 720 780 840 900 924 600 684 744 804 864 624 CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA 1105 AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT 1165 AGTAATGAATATAAAGGAATGCCAGGAGGAGGAATCTTTATAAAATCCAACTTATTGAC 1225 TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT **AACGGCACTITITIAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC** AACGGCACTTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC TCCTTCTACTCTGATGAGTCACTGCAGTACCCCAAAGACTGTACGGGTTCCATATCCAAAG 805 TACTTGTGTGATGTGACATGGGCAACACAAGAATTTTCTTTGCAGTGGCTCAGGAGG **ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAAC** 1081 AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT GTGTCATTCAGTAAAGAGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC CTCTATACTCTACACAGCAGCGTGAATGATAAAGGGCTGAGAGTCCTGGAAGACAATTCA ACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTCTCCA TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA GCAGGAGCTGTGAATCCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA GTCACCAATGCAACTTCCATACAAATCACTGCTCCTGCTTCTATGTTGATAGGGGATCAC TACTTGTGTGTGTGACATGGGCAACACAAGAAAGAATTTCTTTGCAGTGGCTCAGGAGG 865 ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAAC GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA 1141 AGTAATGAATATAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACTTATTGAC CCAGTGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCA 1345 925 1021 1201 1261 1321 1381 385 445 505 541 265 625 661 685 745 781 841 985 325 421 481 601 721 901 961 361 셤 셤 ò 셤 ઠ ద ò 셤 ò 요 ò 셤 ठे 원 δ 셤 ò 셤 à 셤 δ 셤 Š 요 ઠ 셤 8 유 à 셤 ઠ 셤 8 Š

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                          TTGAATGAAACAAAATTTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAG
                                                            AAATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTC
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                                                                                 AACCTTGACCATTACAGAAATTCAACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTT
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18-APR-2002

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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancersasociated polymucleotides (designated PC genes) that selectively chypridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polymucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals. C from the tissues of various organisms such as humans or other mammals. C diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer. C associated genes are useful for diagnosing or treating prostate cancer. C inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene thorapy, as a vaccine or in antisense applications. ABK92115-ABK92263 represent prostate cancer in antisense applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                    2000US-00733288.
2000US-00733742.
2001US-0263957P.
                                                                                                                                                                         16-MAR-2001; 2001US-0276791P.
16-MAR-2001; 2001US-027688P.
06-APR-2001; 2001US-02892P.
24-APR-2001; 2001US-0286214P.
                                                                                                                                                                                                                                                                                                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC
2001WO-US032045
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Matches 2184; Conservative
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141	RESULT 3 AAL44351 ID AAL44351 XX AC AAL44351; XX TO AAL44351; XX TO AAL44351; XX DE Human dipeptidyl peptidase IV (DPP IV) coding sequence. XX Muman; angiodemic condition; angiotensin converting enzyme; ACE; gene; XX XX XX XX XX XX XX XX XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungicide; antiparasitic; anticonvulsant; neuroleptic; cytostatic; antiparkinsonian; noctropic; neuroprotective; antiasthmatic; infection; antidabetic; hypotensive; nephrotropic; antiarthritic; antinifammatory; gene therapy; epilepsy; schizophrenia; cancer; Parkinson's disease; Alzhaimer's disease; asthma; diabetes; hypertension; arthritis; polycystic Kidney disease; tissue-specific luminally expressed protein; inflammatory bowel disease; enzyme; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue-specific endothelial membrane protein; antibacterial; virucide;
                                                                                     1870 GGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTTCAAAAATGGGATTT
                                                                                                                                                              1930 GTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATG
                                                                                                                                                                                           2050 TGGGAGTACTATGACTCAGTGTACACAGAACGTTACATGGGTCTCCCAACTCCAGAAGAC
                                                                                                                                                                                                                                                      AACCTTGACCATTACAGAAATTCAACAGTCATGAGCAGAGCTGAAAATTTTAAACAAGTT
                                                                                                                                                                                                                                                                GAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCAG
                                                                                                                                                                                                                                                                                                    2230 ATCTCCAAAGCCCTGGTCGATGTTGGAGTGGGATTTCCAGGCAATGTGGTATACTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                 2290 GACCATGGAATAGCTAGCAGCACACCAACCATATATATACCCACATGAGCCACTTC
            AAATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTC
                                   GGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCAGACAATTTTCAAAAATGGGATTT
                                                                                                                                             GTGGACAACAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATG
                                                                                                                                                                                 GTCCTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGAATAGCCGTGGCGCCTGTATCCCGG
                                                                                                                                                                                                                                                                                                                            2041 ATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGTGTATACTGATGAA
                                                                                                                                                                                                                                                                                                                                                               Human liver dipeptidyl peptidase IV (DPP4) encoding cDNA SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                            2350 ATAAAACAATGTTTCTCTTTACCT 2373
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The present invention describes a method (M1) for delivering an therapeutic agent to a specific tissue, comprising administering an amount of a therapeutic complex comprising a digad which binds to a computation of the bissue-specific luminally expressed protein, a therapeutic group, and linker which links the group to the ligand. Tissue-specific endothelial nembrane proteins from the present invention can have antibacterial, circuide, fungicide, antiparasitic, anticonvulsant, neuroleptic, virucide, fungicide, antiparasitic, anticonvulsant, neuroleptic, orticatic, antiparkinsonian, nootropic, neuroprotective, antiasthmatic, antidiabetic, hypotensive, nephrotropic, antiarthritic and antidiabetic, hypotensive, nephrotropic, antiarthritic and antidiabetic, hypotensive, nephrotropic, antiarthritic and antistensulate complex may be used to treat or diagnose any disease for therapeutic complex may be used to treat or diagnose any disease for which a tissue- or organ-specific treatment would be efficacious, such as in cases of infections (e.g. bacterial, viral, fungal and parasitic), epilepsy, schizophrenia, cancer, Parkinson's disease, Alzheimer's arthritis, and inflammatory bowel disease. The present sequence encodes a human liver dipeptidyl peptidase IV (DPP4), which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                               Delivering a therapeutic agent (e.g. immunosuppressant) to a specific tissue, comprises administering an amount of a therapeutic complex comprising a therapeutic group, a ligand that binds to a tissue-specific protein, and a linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC
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100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                                                                                                                                           (TARG-) TARGET PROTEIN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 24; Page 102-105; 123pp; English
                                                                       08-JUN-2001; 2001US-0297021P.
07-JUN-2002; 2002WO-US018185
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P-PSDB; ABP56700.
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                                                                                                                                                                                                                                                                                                                                The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase cotivity or members of the protein tyrosine kinase cotivity or members of the protein tyrosine kinase correlating the activity of cells, comprising obtaining a sample of cells, concellating the activity of the cells, comprising a sample of cells, correlating the expression of the markers to the compound's ability to correlate the activity of the cells, (2) a plurality of cell innes for identifying polynuclectides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polynuclectides and collypeptides that predict compound sensitivity or resistance of cells associated with a disease state, compounds ensitivity or resistance of cells compounds, analysing the expression pattern of a microarray of polynuclectides or polypeptides, and selecting the polynuclectides or polypeptides, and selecting collypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynuclectides and polypeptides are useful in predicting the compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized cancer; based on patient resistion of the present invention.
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                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 34; 139pp; English
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                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO
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Best Local Similarity 100.0%;
Matches 2184; Conservative 0;
                                                                  18-JAN-2002; 2002US-0350061P.
                                   17-JAN-2003; 2003WO-US001981
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31-JUL-2003
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

Claim 8; SEQ ID NO A203; 1385pp; English.

Hevezi PA; A;

Gish KC, Glynne R, Wilson KE, Zlotnik

Aziz N, Ginsburg WM, Murray R, Watson SR,

Afar D, A Mack DH,

WPI; 2003-468649/44. P-PSDB; ADN39604.

(EOSB-) EOS BIOTECHNOLOGY INC

09-SEP-2002; 2002US-0409450P

22-JUL-2002;

2002US-0347211P. 2002US-0347349P. 2002US-0355250P. 2002US-0356714P.

08-JAN-2002; 10-JAN-2002; 08-FEB-2002; 13-FEB-2002;

20-FEB-2002; 29-MAR-2002; 12-APR-2002; 05-JUN-2002;

2002US-0368809P 2002US-0370110P 2002US-0372246P 2002US-0386614P 2002US-0396839P 2002US-0397775P 2002US-0397845P

2001US-0335394P 2001US-0340376P

03-DEC-2001; 14-DEC-2001;

-NOV-2001;

13-NOV-2002; 2002WO-US036810

WO2003042661-A2.

22-MAY-2003

Homo sapiens.

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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases auch as angioganic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a content on the invention or by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; use of such antibodies for drug targeting; polypeptide of the invention; use of such antibodies for drug targeting; cand methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating antibodies and other conditions such as psoriasis, ischemaia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
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Best Local Similarity 100.
Matches 2184; Conservative
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ADN39603 standard; cDNA; 3407 BP.

RESULT 6 ADN39603 17-JUN-2004 (first entry)

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ADN39603;

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0; Gaps

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Page 10

us-10-659-055-2.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolyvic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropiaty. This sequence represents a human PRO polynucleotide of
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100.0%; Score 2184;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2184; Conservative 0; Mismatches
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                                                                                     Human PRO polynucleotide #165.
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Wood WI,
  ADO19399;
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Dipeptidyl-peptidase IV; DPP4; cardiovascular disease; dermatological disease; cancer; neoplasm; hematological disease; respiratory disease; gastrointestinal disease; liver disease; metabolic disorder; Cardiovascular-Gen.; Endocrine-Gen.; Antiinflammatory; Gastrointestinal-Gen.; Gynecological; Hepatotropic; Neuroprotective; Cytostatic; Antiparkinsonian; Nootropic; Cardiant; Antiarrhythmic; Antiatteriosclerotic; Antianemic; Antidiabetic; Dermatological; Immunosuppressive; Muscular-Gen.; Antitheumatic; Antiarthritic; Antipsoriatic; Antinfertility; Gene Therapy; gene; 88

"Human DPP4"

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Location/Qualifiers 76. .2376

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oue or uspeptidytpeptidase IV (DPP4) polypeptides or polynucleotides for screening therapeutic agents or for diagnosing or treating diseases associated with DPP4, e.g. cardiovascular, metabolic, inflammatory, or neurological disorders.

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Summer

Brueggemeier U,

Golz S,

2004-834301/82 P-PSDB; ADV25525. GENBANK; NM_001935.

AG.

(FARB) BAYER HEALTHCARE

12-MAY-2004; 2004WO-EP005071. 21-MAY-2003; 2003EP-00011481 Disclosure; SEQ ID NO 1; 128pp; English.

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The present sequence is the coding sequence for human dipeptidyl-

CC peptidase IV (DPP4). The invention relates to novel disease associations

CC DPP4 polypeptides and polynuclectides and to novel methods of

CC screening for therapeutic agents for the treatment of cardiovascular

CC disorders, dermatological disorders, cancer, hematological disorders,

CC disorders and metabolic diseases. Pharmaceutical compositions are

CC disorders and metabolic diseases. Pharmaceutical compositions are

CC provided for treatment of these diseases and disorders and comprise a

CC modulators of DPP4 activity. The therapeutic agent is preferably a small

CC module, an RNA molecule, an antisense oligonuclectide, a polypeptide,

an antibody or a ribozyme. The invention also provides methods of

CC diagnosing diseases and disorders associated with DPP4 by measuring the

CC amount of a DPP4 polynuclectide in a sample and comparing it with the

amount of a DPP4 polynuclectide in a sample and comparing it with the

amount in a sample from a healthy and/or diseased mammal. The disease

CC and disorders include Parkinson's disease, dementia, Alzheimer's disease,

CC disorders, leukemia, panoreattis, Crohn's disease, inflammatory bowel

CC disease, diabetes, Cushing's syndrome, systemic lupus erythematosus,

CC material infare.
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Matches 2184; Conservative
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Human dipeptidyl-peptidase IV coding sequence.

(first entry)

24-PEB-2005

ADV25524;

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ADV25524 Btandard; cDNA; 3407

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as anglogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; antibodies for drug targeting; and methods of screening for modulators of acitivity or expression of the polypeptides and mucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attendance and activation syndromes, activation diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                     Human, differential expression, cancer, angiogenic disorder,
fibrotic disorder, psoriasis, ischaemia, heart disease, atherosclerosis,
                                                                                                                                inflammatory disease; autoimmune disease;
retinal neovascularistaion syndrome; scarring; uterine fibroid;
detection; diagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine; gene; ss.
                                                                            Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:589
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3, Zlotnik A;
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Wilson KE,
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Murray R, Watson SR,
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2001US-033334P
2001US-0343376P
2002US-03476P
2002US-0347211P
2002US-0347349P
2002US-0355250P
2002US-0355250P
ADN39271 standard; cDNA; 2301
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2002US-0370110P.
2002US-0372246P.
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22-JUL-2002; 2002US-0397775P.
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20-FEB-2002;
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29-NOV-2001;
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                                                                                               Gaps
                                                              Length 2301;
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sequence represents a nucleic acid sequence of the invention
                               Sequence 2301 BP; 734 A; 453 C; 492 G; 622 T; 0 U; 0 Other;
                                                                                                   1; Indels
                                                                  DB 11;
                                                              99.9%; Score 2182.4;
99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                   Matches 2183; Conservative
                                                                                   Similarity
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                                                                   Query Match
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The invention relates to a novel crystal of a dipeptidyl peptidase IV (PPPIV) which is sufficient to ensure a resolution capable of analysing its three-dimensional structure up to the side chain level by X-ray crystallographic structural analysis. The crystal of the invention demonstrates immunomodulatory, antidiabetic, antidifiammatory, neuroprotective, antithyroid, antitheumatic, antiarthritic, anti-HIV and cytostatic activities and may be useful for providing a three-dimensional structural coordinate as the information for designing, identifying, evaluating or searching for an effector of the dipeptidyl peptidase IV. The effector may be useful as a modulatory agent of immune response and as a thraspeutic or prophylactic agent for diabetes, inflammation, multiple sclerosis, Grave's disease, chronic rheumatoid arthritis, AIDS or cancer. The current sequence is that of the human full-length colon dipeptidyl peptidase IV (DPPIV) DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .2301
/*tag= a
/product= "Human full-length colon dipeptidyl peptidase
IV (DPPIV) protein"
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2155 ATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAA
                                          GACCATGGAATAGCTAGCAGCACACCACCAACATATATACCCACATGAGCCACTTC
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                                                                                                                                                                                                                                                                                     Human full-length colon dipeptidyl peptidase IV (DPPIV) DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a new microarray which comprises probes for genes involved in psychoneuroendocrinimmune (PNI) activity. The microarray is useful in diagnosing a condition associated with PNI activity, such as CFS, type-2 diabetes, allergic condition, inflammation, cancer and infection. The present sequence represents a psychoneuroendocrinimmune gene expressed sequence tag. Note the specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New microarray comprising probes for genes involved in psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a condition associated with PNI activity, e.g., inflammatory or infectious
                                                                                                                                                                                                                                                                                    microarray; psychoneuroendocrinimmune; chronic fatigue;
non-insulin dependent diabetes; allergy; immune disorder; inflammation;
cancer; neoplasm; infection; expressed sequence tag; ss.
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Nucleotide sequence of a human CD26 protein.

26-AUG-2004

AD071643

ADO71643 ID ADO7 XX ADO AC ADO7 XX ZE-A XX XX XX

BP

ADO71643 standard; DNA; 2461

RESULT 12

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chemotherapeutic or radiocherapeutic agents, is used for the treatment and prevention of cancers. Expression of CD26 enhances the sensitivity of the cancer cell to the chemotherapeutic or radiotherapeutic agent. CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is CD26 topolsomerase II inhibitor. The CD26 composition of the invention is useful for inhibiting the growth of a cell, inducing cell cycle arrest in a cell, killing a cancer cell, potentiating the effect of a chemotherapeutic agent and/or a radiotherapeutic agent on a tumour cell, inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing or enhancing apoptosis of cancer cell, treating cancer, or inducing an entigen-presenting topolsomerase II expression in a cell, for activating an antigen-presenting cell, or for potentiating immune responses of an animal. The present sequence encodes a CD26 protein, and is used to create vectors which are used to produce compositions of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a CD26 composition, and a chemotherapeutic and/or a radiotherapeutic agent for e.g. inhibiting the cell growth, inducing ce.cycle arrest, killing a cancer cell, treating cancer, or inducing tumor regression or tumor necrossis.
CD26; chemotherapeutic; radiotherapeutic; cancer; call growth; dipeptidyl peptidase IV; DPPIV; topoisomerase II inhibitor; call cycle arrest; tumour; tumour necrosis; immune response; human; ss; gene.
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Pred. No. 0;
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                                                                                                                                         Location/Qualifiers
26. .2326
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/product= "CD26"
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colles are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial colls are stimulated with interleukin-13. Also described: (1) a reagent (1) for cesting for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent (C to treat bronchial asthma or chronic obstructive pulmonary disease; (5) a marken gene or an inmal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an antisense mucleic acid corresponding to a portion of the marker gene, a tibozyme, a polynucleotide that suppresses the correspond by a marker gene; and (7) a DNA chip for testing for expression of the gene through an RNA effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for creating for a cremening for a pherapeutic agent for probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for resting for a cremening for a properser. The present
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20-MAR-2003; 2003JP-00077212.
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                        sapiens
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GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA 1304 agraargaararaaaggaargccaggaggaaggaarcrirraaaaarccaacriaagagac 1424 TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT 1484 1261 GTGTCATTCAGTAAAGAGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC 1320 ractrigricaricracardigecaacacaaaaaaaaaarrircririgeagrigecreagagg 1064 AAAGGCACCTGGGAAGTCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT 1364 780 360 480 9 99 720 464 584 420 704 764 824 884 CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA ACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGTGTGGTGGTCTCCA recriciacicidatoagicacideagiacecaaagacidiaceggirecaiaiceaaag ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAAC CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACTTTAAAAT AACGGCACTTTTTTAGCATATGCCCAATTTTAACGACACAGAAGTCCCACTTATTGAATAC AGTAATGAATATAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACTTATTGAC CCAGTGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCA ACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTCTCCA TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTAAATACAGACTCTCTCAGCTCA GTCACCAATGCAACTTCCATACAAATCACTGCTCCTGCTTCTATGTTGATAGGGGATCAC TACTTGTGTGATGTGACATGGGCAACACAAGAAAGAATTTCTTTGCAGTGGCTCAGGAGG GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT CCAGTGGGTCATAAATTGGCATATGGAACAATGACATTTATGTTAAAATTGAACCA GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCAGCTCA 1005 1065 1125 1185 1021 1245 1081 1305 1141 1365 1201 1425 465 525 585 825 945 841 961 405 241 301 361 421 645 481 705 541 765 601 199 885 721 781 901 셤 ઠે a 8 ď ò 셤 ઠે 셤 Š g ઠ g ઠે g 8 g ò 셤 ઠે 셤 ò 셤 ò 셤 ⋧ 원 ò 셤 ð 원 ઠે 음 δ 유 ö 120 AGTOGOAAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATAC 284 rccrraagarggarricagarcargaararcrcracaagaaaaaaaaararcrrggra 344 TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT 180 **AGTOGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC** Gaps ; DB 12; Length 3445; 1; Indels Score 2182.4; I Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 99.9%;
Matches 2183; Conservative

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Human; PRO; gene; as; immune related disorder;
systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
vasculitis; sarcoidosis; autoimmune haemolyric anaemia;
autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
renal disease; demyelinating disease; central nervous system;
peripheral nervous system; demyelinating polyneuropathy;
chilain_abarre syndrome;

chronic inflammatory demyelinating polyneuropathy

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Chiu H, Schoenfeld J, Williams

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Dennis K, (Wu TD;

Fong S, I Wood WI,

WPI; 2004-420067/39.

(GETH) GENENTECH INC

06-NOV-2003; 2003WO-US035268 08-NOV-2002; 2002US-0425235P.

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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel PRO polypeptide e.g., PRO69614, PRO711106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or spondyloarthropathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3445 BP; 1085 A; 689 C; 721 G; 950 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 340; 1731pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 2183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADO19398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
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BP

standard; cDNA; 3445

ADO19397

RESULT 14 ADO19397 ADO19397

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Human PRO polynucleotide #164.

(first entry)

12-AUG-2004

1381 GCTTTGGATAMATGCTGCAGAATTGCCAGCCTCCAAAAACTGGACTTCATTTTT 1410 1665 GCTTTGGATAMATGCTGCAGAATTGCCACCTCCAAAAACTGGACTTCATTTTT 1664 1665 GCTTTGGATAAATTGCTGCAGAATTGCCCTCCCTCCATTTTGATAAACCAACTATTTTT 1664 1725 AAATACCTCTACATTGATCACATTGCACTCCACTCCATTTTTTAAATCCACCACTTTTTTTAATCCACACACACACTTTTCCACACACACACACTTTTTT	RESULT 15 AD071613 standard; DNA; 3445 BP. XX AD071613; XX DT 26-AUG-2004 (first entry) XX XX XX XX XX XX XX XX XX XX XX XX XX
3524 360 584 420 644 480 704 704 660 884 660 884 600 1004 1104 11124 11184 11304	1141 AGTNATGATATAAAGGAATGCCAGGAGGAATCTTTATAAAATCCAACTTATTGAC 1200

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The specification describes a CD26 composition which, in conjunction with chemotherapeutic or radiotherapeutic agents, is used for the treatment and prevention of cancers. Expression of CD26 enhances the sensitivity of the cancer cell to the chemotherapeutic or radiotherapeutic agent. CD26 is a dipeptidyl peptidase IV (DPPIV). The chemotherapeutic agent is a copoisonerase II inhibitor. The CD26 composition of the invention is useful for inhibiting the growth of a cell, inducing cell cycle arrest in a cell, killing a cancer cell, potentiating the effect of a chemotherapeutic agent and/or a radiotherapeutic agent on a tumour cell, inducing or enhancing apoptosis of a cancer cell, treating cancer, or inducing tumour regression or tumour necrosis. The CD26 composition is further useful for increasing topoisomerase II expression in a cell, for activating an antigen-presenting cell, or for potentiating immune response of an animal. The present sequence encodes a CD26 protein, and is useful.
                                                                                                                                                                                                                                                                                                                                                                                      Use of a CD26 composition, and a chemotherapeutic and/or a radiotherapeutic agent for e.g. inhibiting the cell growth, inducing celcycle arrest, killing a cancer cell, treating cancer, or inducing tumor regression or tumor necrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3445 BP; 1085 A; 689 C; 721 G; 950 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 153-157; 182pp; English.
                                 Location/Qualifiers
111. .2411
/*tag= a
                                                                                    /product= "CD26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.08;
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                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
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Matches 2183; Conservative
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P-PSDB; ADO71612.
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inducing cell

120 180 240 284 344 300 404 464 524 9 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGTTTT GGACATICTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTTTAGAATAC AACTACGTGAAGCAATGGAGGCATTCCTACACAGCTTCATATGACATTTATGATTTAAAT **AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC** TTCAATGCTGAATATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT GGACATICIATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC AACTACGTGAAGGAATGGAGGCATTCCTACACACTTCATATGACATTTATGATTTAAAT Gaps Length 3445; ö 1; Indels 285 225 405 241 61 121 345 181 465 셤 셤 윰 ò ઠે 셤 ઠે 8 셤

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1124 1184 1020 1244 1080 1304 1140 1364 1200 1424 1260 1484 1320 1544 1380 1440 1004 1064 1604 720 780 840 900 420 480 540 884 960 584 704 764 600 824 999 944 GCTTTGGATAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT ACTGACTGGGTTTATGAAGAAGGTCTTCAGTGCCTACTCTGCTCTGTGTCTCCCA TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA GTCACCAATGCAACTTCCATACAAATCACTGCTTCCTGCTTCTATGTTGATAGGGGGATCAC GTCACCAATGCAACTTCCATACAAATCACTGCTCCTGCTTCTATGTTGATAGGGGATCAC 1065 ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGATGAATCGGTGGAAGATGGAAC CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA AGTAATGAATATAAAGGAATGCCAGGAGGAAGGAATCTTTATAAAATCCAACTTATTGAC CTCTATACTCTACACACACAGCGTGAATGATAAAGGGCTGAGAGGTCCTGGAAGAAGATTCA CCAGIGGGICATAAATIGGCATAIGITIGGAACAATGACATITAAGITAAAATIGAACCA ACTGACTGGGTTTATGAAGAGGAAGTCTTCAGTGCCTACTCTGCTCTGTGGTGGTCTCCCA AACGGCACTTTTTTAGCATATGCCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC TACTTGTGTGATGTGACATGGGCAACACAGAAAGAATTTCTTTGCAGTGGCTCAGGAGG 1005 TACTIGIGAGATGIGACAIGGGCAACACAAGAAAGAATTICTITIGCAGIGGCTCAGGAGG ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGATGAATCCAGTGGAAGATGGAAC CCTTCAGAACCTCATTTTACCCTTGATGGTAATAGCTTCTACAAGATCATCAGCAATGAA GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT GTGTCATTCAGTAAAGAGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC GTGTCATTCAGTAAAGAGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC CTCTATACTCTACACAGCGTGAATGATAAAGGGCTGAGAGTCCTGGAAGACAATTCA 885 1185 525 585 645 481 705 541 765 825 945 1125 1245 1081 1305 1141 1365 1425 361 421 601 661 781 841 961 1021 1201 1485 1545 721 901 1261 1321 1381 셤 ઠે 셤 셤 ઠે 셤 ઠે 요 ሯ 요 ठ 셤 ò q 요 g 셤 g g 셤 ò ò ઠ ઠ ò ò ð ઠે 셤 δ 셤 셤 ò ∙ &

Search completed: February 17, 2006, 04:54:26 Job time : 1321 secs

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03-JUN-2004
                   AB023952 Felis cat
AF461806 bos tauru
AY056814 Bos tauru
AY198323 Sus scrof
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CG777283 Sequence
AX401894 Sequence
J04591 Rat bile ca
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BC082401 Xenopus I
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AX33666 Sequence
AX33466 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
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I32308 Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hennig, M., Loeffler, B.M. and Thoma, R.
Crystal structure of dipeptidyl peptidase IV
Patent: BF 142293-A 1 26-MAY-2004;
F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers

    .2211
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/db_xref="taxon:9606"

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Sequence 1 from Patent BP1422293.
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AX401944

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AB158225

AB158226

AB158229

AB158239

AB158239

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AB158239

AB158239

AB15823
                       AB023952
AF461806
AY056834
AY198323
CQ777283
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CQ815921
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AR653630 Sequence
X60708 Human pcHDP
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CS041831 Sequence
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MC65265 Homo sapi
CS134667 Sequence
AR380481 Sequence
                                                                                                                           February 17, 2006, 04:24:53; Search time 11140 Seconds (without alignments) 11144.174 Million cell updates/sec
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                   5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                        5883141 seqs, 28421725653 residues
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                   version 5
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Maximum Match 100%
Listing first 45 summaries
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361 CCAGT 385 CCAGT	CCAGTGGGTCATAAATTGGCATATGTTTGGAACAATGACATTTATGTTAAAATTGAACCA 420 	1465 TIGAATGAAAGAAAATTIGGIAJCAGGAGGATGATCTIGCCTCCTCATTITGATAAATCCAAG
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781 TAC	3GAGG	Qy 1861 TGGGAGTACTATGACTCAGTGTACACAGAACGTTACATGGGTCTCCCAACTCCAGAGAC 192.
		OY 1921 AACCTTGACCATTACAGAAATTCAACAGTCATGAGGCTGAAAATTTTAAACAAGTT 1980
901 TGC 925 TGC	TTAGG	
961	TGAA	
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1141 AGT 1165 AGT	agtaatgaatataaaggaatgccaggaggaaggaatctttataaaatccaagttattgac 1200 	RESULT 2 CQ963950 LOCUS CQ963950 3407 bp DNA linear PAT 13-DEC-2004
1201 TAT	TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT 1260 	
1261 GTGT 	GTGTCATTCAGTAAAGAGGGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC 1320	SOURCE Homo Baptens (numan) ORGANISM Homo Bapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

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OY 1921 AACCTTGACCATTACAGAATTCAACAGTCATGACGCTGAAAATTTTAAACAGT 2169 Db 2110 AACCTTGACCATTACAGAAATTCAACAGTCATGACGCTGAAAATTTTAAACAGT 2169 Cy 1991 GAGTACCTCCTTATTCATGAAACAGTGATGATAACAGTTTAACAGTT 2169 Cy 1991 GAGTACCTCCTTATTCATGAAACAGCAGATGATTACACTTTCAGCAGTCAGT	Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Description (0.0) 1 AGTCGCAAACTTACTCTAACTCATTACTCTAAAAATACTTATAGACTCAAGTTATAC 60 Db 190 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAAATACTTATAGACTCAAGTTATAC 249 Qy 121 TTCAATGCTGAATATGGAACAGTCATTACTTACAACAACAACAAAAAAAA

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Db 1870 GGAACATTTGAAGTTGAAGATCAAATTGAAGCAGCCAGACAATTTTCAAAAATGGGATTT 1929	Qy 181 GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATTCTCTTAGAATAC	TAGAATAC 240
Qy 1741 GTGGACAACGAATTGCGGCTGGTCGTATGGGGGTACGTAACCTCAATG 1800	Db 370 GGACATICTATCAATGATTATICAATATCTCCTGATGGGCAGTTTATICTCT	TAGAATAC 429
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QY 1801 GTCCTGGGATCGGGAAGTGGCGTGTTCAAGTGTGGAAATAGCCGTGGCGCCTGTATCCCGG 1860	Db 430 AACTACGTGAAGGAAGGCATTCCTACACACGCTTCATATGACATTTAAAT	
Db 1990 Greensancescandescandescararicas paragrandes and 1990 Greensances 2049	Qy 301 AAAAGGCAGCTGATTACAGAAGAGAGTTCCAAACAACACAGGGGGGTC	CATGGTCA 360
Qy 1861 TGGGAGTACTATGACTCAGTGTACACAGTACGTTACATGGGTCTCCCAACTCCAAGAC 1920	Db 490 AAAAGCCAGCTGATTACAGAAGAGAGGATTCCAAACAACACACAC	CATGGTCA 549
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RESULT 4	Db 850 GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTAGTACAGACTCTC	rcaecrca 909
AR653630 3407 bp	Qy 721 GTCACCAATGCAACTTCCATACAAATCACTGCTTCTATGTTGATAGGGGATCAC	3GGATCAC 780
DEFINITION Sequence 5 from patent US 6887679. ACCESSION AR653630	Db 910 GTCACCAATGCAACTTCCATACAAATCACTGCTCCTGCTTCTATGATAC	secarcac 969
VERSION AR653630.1 GI:67584135 KEYWORDS .	Qy 781 TACTTGTGATGTGACATGGGCAACACAAGAATTTCTTTGCAGTGGCTCAGAGG	rcaggagg 840
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,	Qy 841 ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGAATCCAGTGGAAGATGGAA	SATGGAAC 900
AUTHORS Brown, J. Address of Co. 310// AUTHORS Brown, J. TITLR Mathods for identifying contraindications to angiotensia contexting	Db 1030 ATTCAGAACTATTCGGTCATGGATATTTGTGACTATGAATCCAGTGGAAGAACC	ATGGAAC 1089
enzyme inhibitor and/or vasopeptidase inhibitor treatment AL Patent: US 6887679-A 5 03-MAY-2005;	Qy 901 IGCTTAGTGGCACGCAACACATTGAAATGAGTACTACTGGCTGG	SATTTAGG 960
	Db 1090 TGCTTAGTGGCACGCAACACATTGAAATGAGTACTACTGGCTGG	SATTTAGG 1149
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	Qy 1021 GAAGGTTACAGACACATTTGCTATTTCCAAATAGATAAAAAAGACTGCACATTTATTACA	TTATTACA 1080

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  PRI 16-NOV-1993
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Direct Submission
Submitted (30-JUN-1991) Y. Misumi, Second Dept of Biochemistry, Submitted (30-JUN-1991) Y. Misumi, Second Dept of Biochemistry, Submitted (30-JUN-1991) Y. Misumi, Second Dept of Medicine, Fukuoka University, 7-45-1 Nanakuma Jonnan-ku, Fukuoka 814-01, JAPAN
On Aug 11, 2005 this sequence version replaced gi:251771.
See Ann. Hum. Genet. 54:191-197(1990) for overlapping sequence.
Location/Qualifiers
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misumi,Y., Hayashi,Y., Arakawa,F. and Ikehara,Y.
Molecular cloning and sequence analysis of human dipeptidyl
peptidase IV, a serine proteinase on the cell surface
Biochim. Biophys. Acta 1131 (3), 333-336 (1992)
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100.0%; Score 2184;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2184; Conservative 0; Mismatches
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dipeptidyl peptidase IV; pcHDP7.
Homo sapiens (human)
Homo sapiens
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Hiramateu, H., Kyono, K., Shima, H. and Sugiyama, S.
Three-dimensional structure of dipeptidyl peptidase
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| // db_xref="taxon:9606"
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L. Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: i Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18765693. Location/Qualifiers
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KLAYVWNNDIYVKIBPNLESYRITWYGKBDIIYNGTTDWYVEBEVFGAYSALKWSPNG
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WNCLVARQHIEMSTTGWYGRFRPSEPHFTLDGNSFYKIISNEGSYRHICYFQIDKXDC
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DYLKNTYRLKLYSLRWISDHEYLYKQENNILVFNAEYGNSSVFLENSTPDEFGHSIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R.
Direct Submitseion
Submitted (31-AUG-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 16, 2003 this sequence version replaced gi:15426453. Contact: MCC help desk Email: cgapbs-r@mail.nih.gor. Tissue Procurement: CLONTECH CLONTECH CLONTECH CLONTECH CLONTECH CLONTECH Laboratories, Inc. CLONTECH Laboratories, Inc. CLONTECH Laboratories, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadams@systemsbiology.org contact: amadams@systemsbiology.org Anup Madan, Jessica Rahay, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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On Sep 16, 2003 this sequence version replaced gi:15426453
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/organism="Homo sapiens"
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1 (Dasse 1 to 2431)
Straugherg, R.L., Fingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heleh, F.,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1915 GTCCTGGGAATGGGGAAGTGGGGGTGTTCAAGTGTGGAAATAGCCGTGGCGCCTGTATCCCCGG
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                              TTGAATGAAACAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAG
                                                                                  TTGAATGAAACAAAATTTTGGTATCAGATGATCTTGCCTCCTCATTTTGATAAATCCAAG
                                                                                                                                                                                                     1615 AAATATCCTCTACTATTAGATGTGTATGCAGGCCCATGTAGTCAAAAAGCAGACACTGTC
                                                                                                                                                                                                                                                                                                       GTGGACAACAAACGAATTGCAATTTGGGGCTGGTCATATGGAGGGTACGTAACCTCAATG
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OY 1921 AACCTTGACCATTACAGAAATTCAACAGTCATGAGCTGAAAATTTTAAACAAGTT 1980 2030 AACCTTGACCATTACAGAAATTCAACAGCAGAGCTGAAAATTTTTAACAAGTT 2089 2030 AACCTTGACCATTACAGAAATTCAACAGCAGAGCTGAAAATTTTTAACAAGTT 2089 1981 GAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCACTTTCAGCAGTCAGCTCAG 2040 2090 GAGTACCTCCTTATTCATGGAACAGCAGATGATAACGTTCAACTTTCAGCAGTCAGCTCAG 2149 2091 ATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAA 2100 2150 ATCTCCAAAGCCCTGGTCGATGTTGGAGTGGATTTCCAGGCAATGTGGTATACTGATGAA 2209 2101 GACCATGGAATAGCTTGACGACACACACATATATATATACCCACATGAGCCACTTC 2160 2210 GACCATGGAATAGCTTACCT 2184 OY 2161 ATAAAACAATGTTTCTCTTTACCT 2184 DD 2270 ATAAAAACAATGTTTCTCTTTACCT 2293	RESULT 8 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 CQ727953 VERSION CQ727953 CQ72795 CQ72795 CQ72795 CQ7279	Ouery Match Query Match Best Local Similarity 99.9%; Score 2182.4; DB 6; Length 3411; Best Local Similarity 99.9%; P. Mismatches 1; Indels 0; Gaps 0; Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 1 AGTCGCARAACTTACACTCAATACTTAAAAAAATACTTATAGACTGAAGTTATAC 60 191 AGTCGCARAACTTACACTCAATACTGATTACTTAAAAAATACTTATAGACTGAAGTTATAC 250 Oy 61 TCCTTAAGATGATTACACTCAAACTGATTACTTACAAAAATACTTATAGACTGAAGTTATAC 250 Oy 121 TTCAATGCTGAATATGGAAACAGCTCAGTTTCTTGCAGAAATAATATTCTTGATGATT 370 Oy 121 TTCAATGCTGAATATGGAAACAGCTCAGTTTCTTGCAGAACAGTACATTTGATGAGTTT 370 Oy 181 GGACATTCTATCAATATTATATATATATTCTCTTAGAATAC 430 Oy 241 AACTACGTGAAGGAGTTATTCTACAATACTATAGACTTTAAAT 300 Oy 241 AACTACGTGAAGGAGTTCTTACAATACTCCTGATGGCATTTATATATTTTAAAT 300 Oy 241 AACTACGTGAAGGAGTTCCTACACAGCTTCATATGACTTTAAAT 300 Oy 10 AAAAGGCAGCTGAATTCAATATCCTACACAGCTTCATATGATTTAAAT 490 Oy 301 AAAAGGCAGCTGAATTCAAAACAAACAACACACACAGTCATTATGATTTAAAT 490

765 AACGGCACTTTTTAGCATATGCCCAATTTAACGACACAGAAGTCCCACTTATTGAATAC 824 601 TCCTTCTACTCTGATGAGTCACTGCAGTACCCAAAGACTGTACGGGTTCCATATCCAAAG 660	661 GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCAGCTCA 720	901 TGCTTAGTGGCACGCAACACTTGAAATGACTACTGGCTGG	1081 AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT 1140 1305 AAAGGCACCTGGGAAGTCATCGGGATAGAAGCTCTAACCAGTGATTATCTATACTACATT 1364 1141 AGTAATGAATATAAAAGGAATGCCAGGAGGAAGCAATTATATAAAATCCATTT 1364 1141 AGTAATGAATATAAAAGGAATGCCAGGAGGAAGCAATCTTATAAAAATCCAACTTATTGAC 1200 1365 AGTAATGAATATAAAAGGAATGCCAGGAAGGAATCTTTATAAAATCCAACTTATTGAC 1424	1201 TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT 1260 1425 TATACAAAAGTGACATGCCTCAGTTGTGAGCTGAATCCGGAAAGGTGTCAGTACTATTCT 1260 1261 GTGTCATTCAGTAAAGGGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC 1320 1485 GTGTCATTCAGTAAAGAGCGAAGTATTATCAGCTGAGATGTTCCGGTCCTGGTCTGCCC 1544 1321 CTCTATACTCTACACAGCAGCAGAATATATAACAGGGTTGAGAGTCCTGGGTTGCCT	CTCTATACTTACACACACACACATAAAAGGGCTGAGAGTCCTGGAAGACATTCA GCTTTGGATAAAATGCTGCAGAATGCCCCCCCCCAAAAACTGGACATTCAT GCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT GCTTTGGATAAAATGCTGCAGAATGTCCAGATGCCCTCCAAAAAACTGGACTTCATTATT TTGAATGAACAAAATTTTGGTATCAGATGACCTTGCCTCCCAAAAAACTGGACTTCATTATT	1665 TTGAATGAAAATTTTGGTATCAGATGCTTTTTGCTTTTTTGATAATCCAAG 1724
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285 TCCTTAAGATGGATTTCAGATATCTCTACAAACAAGAAATAATATCTTGGTA 344 121 TTCAATGCTGAATAATGGAAACAGCTCAGTTTTCTTGGAGAACAGTACATTTGATGAGTTT 180 345 TTCAATGCTGAATAATGGAAACAGCTCAGTTTTCTTTGAGAACACTTTGATGAGTTT 1404 181 GGACATTCTATCAATGATTATTCAATATCTCCTGATGGGCAGTTTATCTCTTAGAATAC 2464 241 AACTACGTGAAGCAATGAGAAGACGCATCCTGATGGGCAGTTTATCTCTTAGAATAC 1644 242 AACTACGTGAAGCAATGAGAAGACGAATCCTAACACACAC	GCAGGAGCTGTGAATCCAACTGTAAAGTTCTTTGTTGTAAATACAGACTCTCTCAGCTCA 240 220 2
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Genentech, Inc. (US)
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  Sequence 2385 from Patent WO2005019258.
                                                                                                                                                                                                                                                                              ; Score 2182.4;
; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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CS041831.1 GI:61849188
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Matches 2183; Conservative
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapba-remail.inh.gov
Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Buiffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantipop,S., Thochman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 140 Row: 1 Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18765693. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / translation="mktpwkvllgllgaralvtiitvpvvllnkgtddatadsrktyt
Lidylknytkklyslkup sdheylykgenniivprakygasyrleerhsi
ndysispdgopillenykkgwrhsytagkdiiteriibnsykywspy
Ghklaywnndiyklebnlesyriitwigksdiiyngiidwyeeevpsaxsalwwsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGTELAYAQENDTEVPLIEYSPYSDESLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSL
SSVTNATSIQITAPASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESS
GRWNCLVARQHIEMSTTGWVGRFRPSEPHFTLDGNSFYKIISNEEGYRHICYFQIDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCTFITKGTWEVIGIBALTSDYLYYISNEYKGWPGGRNLYKIOLSDYTKVTCLSCELN
BREQOYYSVESKERAKTYOLRSGPGFDLYTLIASSVUNKGLRTLENDALDKHLONVO
MPSKKLLDFILLNETKWYOMILPPHENKSKKYPLLLUYYAGPCSQKADTVFRLNWATY
LASTENIIVASPDGRGSGYQGDKIMHAINRRLGTFEVEDQIEAARQFSKMGFVDNKRI
ARGRSYGGYTTSMYLGSGYVCGIAVAPVSRWEYYDSYTTERYMGLETPEDNLDH
YRNSTVMSRABNFROYSYLLINGTADDNVHFQQSAQISKALUDVGVDFQAMWYTDEDH
GIASSTAHQHIYTHMSHFIKQCFSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 AGTCGCAAAACTTACACTCTAACTGATTACTTAAAAATACTTATAGACTGAAGTTATAC 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1.3913
| gene="DPP4"
| note="synonyms: ADCP2, CD26, DPPIV, ADABP, TP103"
| db xref="GeneID:1803"
| db xref="MIM:102720"
| 562. .2862
| gene="DPP4"
| codon start=1
| product="dipeptidylpeptidase IV"
| product="dipeptidylpeptidase IV"
| db xref="GeneID:1803"
| db xref="GeneID:1803"
| db xref="MIM:102720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.9%; Score 2182.4;
99.9%; Pred. No. 0;
iive 0; Mismatches
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Best Local Similarity 99.9
Matches 2183; Conservative
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     REMARK
COMMENT
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